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☐ 1. Document ID: US 5770389 A

L9: Entry 1 of 11 File: USPT Jun 23, 1998

US-PAT-NO: 5770389
DOCUMENT-IDENTIFIER: US 5770389 A

TITLE: Apparatus and method for determining the quanity of an analyte in a biological sample by means of transmission photometry

DATE-ISSUED: June 23, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ching; Shan-Fun	Libertyville	IL	N/A	N/A
Helper; Joanell Veronica	Arlington Heights	IL	N/A	N/A
Stimpson; Donald Irvine	Gurnee	IL	N/A	N/A
Gordon; Julian	Lake Bluff	IL	N/A	N/A

US-CL-CURRENT: 435/7.92; 250/214A, 250/214LS, 250/214RC, 250/214SW, 356/432, 356/436, 356/434, 377/12, 377/23, 377/53, 377/58, 422/56, 422/57, 422/82.05, 422/82.08, 435/287.1, 435/287.2, 435/287.7, 435/810, 436/514, 436/518, 436/805, 436/810

ABSTRACT:

A device and method for quantitative determination of an analyte in a biological sample utilizes a non-transparent support medium for retaining a chromatogenic reaction product with the medium being exposed to a source of light for transmitting therethrough a scattered, uniform response light signal which is collected at a photosensitive device whereby the amount of the analyte is correlated to the intensity of the response light signal. The response light signal may be converted to a time-duration signal proportional to light intensity to facilitate the quantitative determination.

38 Claims, 6 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw Desc | Image

☐ 2. Document ID: US 5573909 A

L9: Entry 2 of 11 File: USPT Nov 12, 1996

US-PAT-NO: 5573909
DOCUMENT-IDENTIFIER: US 5573909 A

TITLE: Fluorescent labeling using microparticles with controllable stokes shift

DATE-ISSUED: November 12, 1996

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Singer; Victoria L.	Eugene	OR	N/A	N/A
Haugland; Richard P.	Eugene	OR	N/A	N/A

US-CL-CURRENT: 435/6; 435/5, 435/7.1, 436/172, 436/518, 436/528, 436/531, 436/532, 436/533, 436/534, 436/546, 436/805

ABSTRACT:

The invention relates to methods for labeling or detecting one or more target materials using surface coated fluorescent microparticles with unique characteristics. The unique microparticles used to practice the invention have at least two components: an external substance or coating that is selective for each target material and an internal mixture of multiple fluorescent dyes. The mixture of dyes is a series of two or more fluorescent dyes having overlapping excitation and emission spectra allowing efficient energy transfer from the excitation wavelength of the first dye in the series, transfer through the dyes in the series and re-emitted as an optical signal at the emission wavelength of last dye in the series, resulting in a desired effective Stokes shift for the microparticle that is controlled through selection of appropriate dyes. The unique microparticles are combined with a sample thought to contain the target material(s), so that the microparticles label the target materials. The sample is then optionally illuminated, resulting in fluorescence of the microparticles that is used to detect one or more target materials.

30 Claims, 11 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 6

3. Document ID: US 5326692 A

L9: Entry 3 of 11 File: USPT Jul 5, 1994

US-PAT-NO: 5326692
DOCUMENT-IDENTIFIER: US 5326692 A

TITLE: Fluorescent microparticles with controllable enhanced stokes shift

DATE-ISSUED: July 5, 1994

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Brinkley; John M.	Elmira	OR	N/A	N/A
Haugland; Richard P.	Eugene	OR	N/A	N/A
Singer; Victoria L.	Eugene	OR	N/A	N/A

US-CL-CURRENT: 435/6; 252/301.34, 252/301.35, 428/402, 435/7.92, 436/518, 436/523, 436/529, 436/531, 436/546, 436/805

ABSTRACT:

The invention relates to microparticles incorporating a series of two or more fluorescent dyes having overlapping excitation and emission spectra allowing efficient energy transfer from the excitation wavelength of the first dye in the series, transfer through the dyes in the series and re-emitted as an optical signal at the emission wavelength of last dye in the series, resulting in a desired effective Stokes shift which is controlled through selection of appropriate dyes.

15 Claims, 4 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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☐ 4. Document ID: US 4918004 A

L9: Entry 4 of 11 File: USPT Apr 17, 1990

US-PAT-NO: 4918004
DOCUMENT-IDENTIFIER: US 4918004 A

TITLE: Method of calibrating a flow cytometer or fluorescence microscope for quantitating binding antibodies on a selected sample, and microbead calibration kit therefor

DATE-ISSUED: April 17, 1990

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Schwartz; Abraham	Durham	NC	N/A	N/A

US-CL-CURRENT: 435/7.24; 435/29, 435/34, 435/5, 435/7.21, 435/7.25, 435/810, 435/974, 436/10, 436/510, 436/512, 436/533, 436/534, 436/548, 436/800, 436/811

ABSTRACT:

A method for calibrating a flow cytometer or fluorescence microscope in terms of number of binding antibodies as a function of fluorescence intensity value measured on the flow cytometer or fluorescence microscope, and subsequent measuring of a sample to which the antibodies are bindable. Also disclosed is a microbead calibration kit for carrying out the calibration method of the invention. The disclosed calibration methodology provides a direct relationship between instrument response and numbers of binding antibodies, independent of the fluorochrome employed to label the samples being measured. The method has utility in monitoring the status of an antigenic cellular condition in which the number of antibodies binding to successively obtained cellular samples is determined, to establish the progressionary character of the antigenic cellular condition, in a host from which the cellular samples are taken.

19 Claims, 1 Drawing figures Exemplary Claim Number: 7
Number of Drawing Sheets: 1

☐ 5. Document ID: US 4528131 A

L9: Entry 5 of 11 File: USPT Jul 9, 1985

US-PAT-NO: 4529131
DOCUMENT-IDENTIFIER: US 4529131 A

TITLE: Process and preparation for the quantitative determination of substances able to bind to cerebral receptors and a process for preparing the preparation

DATE-ISSUED: July 9, 1985

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kardos; Julianna	Budapest	N/A	N/A	HUX
Maksay; Gabor	Budapest	N/A	N/A	HUX
Simonyi; Miklos	Budapest	N/A	N/A	HUX

US-CL-CURRENT: 424/570; 436/503, 436/504, 436/545, 436/547, 436/804, 436/815

ABSTRACT:

A process for preparing a stable receptor preparation suitable for the quantitative determination of substances able to bind to cerebral receptors in which a brain or brain-region material is homogenized with an aqueous solution of an inert substance soluble in water; the formed homogenizate is centrifuged at an acceleration of 800 to 1100 g for 8 to 20 minutes to form a supernatant; the brain or brain-region material is isolated from the supernatant by centrifuging the supernatant at an acceleration of 18,000 to 22,000 g for 10 to 20 minutes, the thus-obtained solid substance is rehomogenized in distilled water; the homogenizate is frozen and then thawed and thereafter centrifuged at an acceleration of 7000 to 9000 g for 5-15 minutes; the supernatant is isolated, centrifuged at an acceleration of 35,000 to 45,000 g for 20 to 30 minutes; the obtained solid substance is washed with an aqueous buffer solution of a pH value between 6 and 8, and a suspension consisting of the solid substance and the washing liquid is frozen and then thawed at least once and thereafter the suspension is lyophilized.

8 Claims, 0 Drawing figures Exemplary Claim Number: 1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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☐ 6. Document ID: US RE30627 E

L9: Entry 6 of 11 File: USPT May 26, 1981

US-PAT-NO: RE30627
DOCUMENT-IDENTIFIER: US RE30627 E

TITLE: Apparatus for performing chemical and biological analysis

DATE-ISSUED: May 26, 1981

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bagshawe; Kenneth D.	London	N/A	N/A	GB2
Kemble; James E.	Burgess Hill	N/A	N/A	GB2

US-CL-CURRENT: 436/48; 210/387, 422/101, 422/63, 422/66, 422/71, 436/44, 436/57, 436/808

ABSTRACT:

A system for the automated analysis of large numbers of liquid samples, in which a multiplicity of sample tubes are loaded in racks into a cassette and the loaded cassette is transferred from station to station, with operations of sample insertion, dilution, reagent addition and withdrawal for filtering being performed at successive stations. At each station there is a separate processing module adapted to receive the cassette, each module including the apparatus necessary for performing one of the abovementioned operations on each individual sample tube when it is located at a particular operational location in the cassette. Each module also has members for shifting the racks in the cassette in such manner that all tubes pass through the operational location in turn while strictly maintaining the same order of sequence throughout the operations.

54 Claims, 4 Drawing figures Exemplary Claim Number: 10
Number of Drawing Sheets: 3

☐ 7. Document ID: US 4038150 A

L9: Entry 7 of 11 File: USPT Jul 26, 1977

US-PAT-NO: 4038150
DOCUMENT-IDENTIFIER: US 4038150 A

TITLE: Sample mixing and centrifugation apparatus

DATE-ISSUED: July 26, 1977

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Dorn; Gordon L.	Dallas	TX	N/A	N/A
Hill; Joseph M.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/288.2; 435/30, 604/416

ABSTRACT:

An apparatus for mixing fluids especially suitable for use in laboratory tests for the detection of microbial pathogens which includes an elongated centrifugation vessel, an injectable closure, completely enclosing a treating fluid chamber, and a novel stylus which causes a sample to be admixed and commingled with a treating fluid upon injection. The treating fluid is disposed within the treating fluid chamber and a sterile aqueous solution having a greater density than a sample fluid but able to selectively receive microbial pathogens from the sample fluid is disposed within an evacuated space within the centrifugation vessel. The sample is mixed with the treating fluid when the novel stylus is injected through the injectable closure means facilitating contact of the treating fluid and the sample via an aperture or apertures longitudinally spaced along the stylus so as to be within the treating fluid chamber upon injection of the stylus. The sample-treating fluid mixture then continues its flow through the canalis of the stylus and is deposited on the aqueous solution within the evacuated space of the centrifugation vessel.

53 Claims, 11 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 1

☐ 8. Document ID: US 3932222 A

L9: Entry 8 of 11 File: USPT Jan 13, 1976

US-PAT-NO: 3932222
DOCUMENT-IDENTIFIER: US 3932222 A

TITLE: For isolating pathogenic microorganisms

DATE ISSUED: January 13, 1976

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Dorn; Gordon L.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/289.1; 422/913, 435/30, 435/34, 604/416

ABSTRACT:

A mixing and centrifugation device particularly suitable for use in procedures involving detection of microbial pathogens which includes an elongated enclosed centrifugation receptacle containing an evacuated space and having an injectable closure on an end thereof with an enclosed treating fluid chamber disposed in communication and adjacent the injectable closure and separated from the evacuated space by a thin rupturable membrane. A sample treating fluid is carried within the enclosed treating fluid chamber and a sterile aqueous solution having a greater density than a sample fluid but able to selectively receive microbial pathogens from the sample fluid is disposed within the evacuated chamber. A sample is deposited on the sterile aqueous solution via an injection needle by passing the injection needle through the injectable closure, the enclosed treating fluid chamber, and rupturing the thin membrane such that the sample treating fluid contacts the sample as it passes from the injection needle and is deposited on the liquid filter medium.

24 Claims, 8 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 1

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9. Document ID: US 3928139 A

L9: Entry 9 of 11 File: USPT Dec 23, 1975

US-PAT-NO: 3929139
DOCUMENT-IDENTIFIER: US 3929139 A

TITLE: Detection of microbial pathogens

DATE-ISSUED: December 23, 1975

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Dorn; Gordon L.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/34; 435/30, 435/308.1, 435/36, 435/38, 435/39, 435/822, 435/948, 435/852, 435/873, 435/975, 435/989, 435/985, 435/921, 435/821

ABSTRACT:

A method and apparatus are disclosed which provide for the rapid quantitative detection of microbial pathogens in a sample fluid such as blood. Initially the pathogens are concentrated by depositing the sample fluid on a liquid filter medium such as a concentrated aqueous solution of sucrose or a microporous aqueous solution of a crosslinked polymer having a greater density than the sample, and microporous openings throughout its solubilized network (which range in size between about 1 micron and about 7 microns) and then the material is subjected to centrifugation to cause the pathogens in the sample to selectively pass into the liquid filter medium. This step not only concentrates the pathogens but also separates them from the other components of the sample such as antimicrobial constituents of blood and medicants present in blood samples, such as antibiotics. The liquid filter medium containing the concentrated pathogens is then added to nutrient media for culturing and quantitative counting.

47 Claims, 10 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

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☐ 10. Document ID: US 3875012 A

L9: Entry 10 of 11 File: USPT Apr 1, 1975

US-PAT-NO: 3875012
DOCUMENT-IDENTIFIER: US 3875012 A

TITLE: Apparatus and method for the detection of microbial pathogens

DATE-ISSUED: April 1, 1975

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Dorn; Gordon L.	Dallas	TX	N/A	N/A
Hill; Joseph M.	Dallas	TX	N/A	N/A

US-CL-CURRENT: 435/243; 206/222, 215/247, 215/DIG.3, 422/913, 435/30, 435/309.1, 435/309.2, 435/34, 435/39, 604/415

ABSTRACT:

An apparatus for the isolation and concentration of microbial pathogens from a sample fluid which comprises an elongated enclosed centrifugation receptacle containing an evacuated space in contact with a sterile aqueous solution of a material having a greater density than the sample fluid but able to selectively receive microbial pathogens from the sample fluid, a first injectable closure on one end thereof and a second injectable closure on its other end, and a sterile end chamber in communication with the second injectable closure which contains a sample fluid treating solution together with an injection needle assembly which when actuated will pass through the second injectable closure means and allow communication between the chamber and the evacuated space within the centrifugation receptacle to thereby allow the treating fluid to flow from the chamber into the evacuated space. Thereafter, the sample fluid can be injected into the evacuated chamber of the centrifugation tube through a needle passing through the first injectable closure and allow the sample fluid to admix with the pretreating solution in the evacuated chamber. The article is then subjected to centrifugation to allow the microbial pathogens to selectively pass into the liquid filter medium.

25 Claims, 6 Drawing figures Exemplary Claim Number: 15
Number of Drawing Sheets: 1

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☐ 11. Document ID: US 3825410 A

L#: Entry 11 of 11 File: USPT Jul 23, 1974

US-PAT-NO: 3825410
DOCUMENT-IDENTIFIER: US 3825410 A

TITLE: PERFORMANCE OF ROUTINE CHEMICAL REACTIONS IN COMPARTMENTALIZED CONTAINERS

DATE-ISSUED: July 23, 1974

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bagshawe; Kenneth Dawson	London W 1	N/A	N/A	EN

US-CL-CURRENT: 436/57; 206/459.5, 206/509, 422/101, 422/102, 422/61, 422/66, 422/67, 422/71

ABSTRACT:

In the performance of routine chemical and/or biological reactions, such as saturation analysis using a radioactive marker substance, the standard reactants are dispensed in appropriate amounts, in a prior operation, into a compartmentalized storage container which also constitutes the reaction vessel, the reactants being maintained in a stable unreactive state, such as by freeze drying, until the analysis is to be performed. The reaction is initiated by introduction of a sample to be analysed, whereafter separation of bound and free ligand can be performed either within the compartmentalized vessel itself or externally.

25 Claims, 13 Drawing figures Number of Drawing Sheets: 5

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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☐ 1. Document ID: US 6150089 A

L6: Entry 1 of 3 File: USPT Nov 21, 2000

US-PAT-NO: 6150089
DOCUMENT-IDENTIFIER: US 6150089 A

TITLE: Method and characterizing polymer molecules or the like

DATE-ISSUED: November 21, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Schwartz; David	New York	NY	N/A	N/A

US-CL-CURRENT: 435/6; 204/450, 204/456, 204/600, 204/606

ABSTRACT:

A method for observing and determining the size of individual molecules and for determining the weight distribution of a sample containing molecules of varying size, which involves placing a deformable or nondeformable molecule in a medium, subjecting the molecule to an external force, thereby causing conformational and/or positional changes, and then measuring these changes. Preferred ways to measure conformational and positional changes include: (1) determining the rate at which a deformable molecule returns to a relaxed state after termination of the external force, (2) determining the rate at which a molecule becomes oriented in a new direction when the direction of the perturbing force is changed, (3) determining the rate at which a molecule rotates, (4) measuring the length of a molecule, particularly when it is at least partially stretched, or (5) measuring at least one diameter of a spherical or ellipsoidal molecule. Measurements of relaxation, reorientation, and rotation rates, as well as length and diameter can be made using a light microscope connected to an image processor. Molecule relaxation, reorientation and rotation also can be determined using a microscope combined with a spectroscopic device. The invention is particularly useful for measuring polymer molecules, such as nucleic acids, and can be used to determine the size and map location of restriction digests. Breakage of large polymer molecules mounted on a microscope slide is prevented by condensing the molecules before mounting and unfolding the molecules after they have been placed in a matrix.

16 Claims, 53 Drawing figures Exemplary Claim Number: 1,11
Number of Drawing Sheets: 16

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 6027884 A

L6: Entry 2 of 3 File: USPT Feb 22, 2000

US-PAT-NO: 6027894
DOCUMENT-IDENTIFIER: US 6027894 A

TITLE: Thermodynamics, design, and use of nucleic acid sequences

DATE-ISSUED: February 22, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lane; Michael J.	Baldwinsville	NY	N/A	N/A
Benight; Albert S.	Schaumburg	IL	N/A	N/A
Faldasz; Brian D.	Maynard	MA	N/A	N/A

US-CL-CURRENT: 435/6; 435/5, 536/24.3, 536/24.33

ABSTRACT:

A method of providing the sequence of a single stranded nucleic acid molecule, which, when hybridized to a complementary single stranded molecule, results in a double stranded (duplex) structure having a preselected value for a free energy parameter.

6 Claims, 25 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 11

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw. Desc | Image

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☐ 3 Document ID: US 5654147 A

L6: Entry 3 of 3 File: USPT Aug 5, 1997

US-PAT-NO: 5654147
DOCUMENT-IDENTIFIER: US 5654147 A

TITLE: Method of hybridization using oligonucleotide probes

DATE-ISSUED: August 5, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wood; William I.	San Mateo	CA	N/A	N/A
Lasky; Laurence A.	Sausalito	CA	N/A	N/A

US-CL-CURRENT: 435/6; 435/5, 435/91.2, 536/24.3, 536/24.32, 536/24.33

ABSTRACT:

An improved method of hybridization with oligonucleotide probes using tetramethylammonium chloride is provided. The method is useful for screening mixtures of DNA sequences, including libraries of high DNA sequence complexity, with a single oligonucleotide probe or a pool of probes representing all possible codon choices for a short amino acid sequence.

5 Claims, 41 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 32

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

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L6: Entry 1 of 3 File: USPT Nov 21, 2000

DOCUMENT-IDENTIFIER: US 6150099 A
TITLE: Method and characterizing polymer molecules or the like

DEPR:
High image quality greatly facilitates image processing. Fluorescence images of DNAs obtained in fluid rather than gel are brighter, sharper and relatively free of fluorescing artifacts. Consequently, they are ideal for unattended image processing since they can be transformed into reliable binary or digital images, which are easily accepted by our processing algorithms. This high throughput sizing methodology can be tested and benchmarked by using a series of Not I digested yeast chromosomes mixtures (containing DNAs 30-900 kb), of increasing complexity. Statistical analysis to calculate the precision of single measurements can be performed and the ultimate accuracy of this methodology determined. Confidence intervals are determined to establish the minimum number of molecules necessary for adequate analysis of complex mixtures. This analysis will help determine the usable size resolution and size discrimination levels. Sources of noise and systematic error are detected and eliminated as much as possible. A lower size limit of 5-20 kb and an increased upper size limit are provided by the present invention since molecules with contour lengths greater than the microscope viewing field are sized by offsetting a known distance from the interface and monitoring only coil ends.

DEPR:
The gel-fluid interface system can be used in this invention to obtain high resolution fluorescence intensity measurements of single molecules. Measurement precision can be increased and lower size limitations made for these measurements. Increased sizing performance accrues from a number of factors, such as, but not limited to, the simultaneous use of three sizing methods will increase precision and accuracy (length, relaxation and intensity); the fluid-gel interface system produces optically flat molecules more consistently than gel fixation; the degree of molecular elongation is more controllable than gel fixation, and the elimination of gel provides sharper, brighter images that are more free of fluorescing artifacts. As mentioned previously, high quality images are easier to image process automatically.

DEPR:
To minimize errors arising from relative intensity measurements, a number of internal standards can be placed into samples so that fluorescence non-linearities arising from uneven illumination can be substantially reduced or eliminated. The internal standard preferably meets several requirements: 1) negatively charged to avoid sticking to DNA; 2) fluorescent in the same absorption and emission wavelengths as the DNA-fluorochrome complex, and 3) readily distinguishable from the test DNA molecules to be measured. Small DNA molecules (20-50 kb) can be used as internal standards. These molecules are dispersed throughout the sample to be measured and preferably react identically as the sample DNA to illumination and electrophoretic conditions (e.g., in free solution). The internal standards to determine relative mass, instead of using contiguous restriction digestion products from the same parental molecule. To optimize these determinations, we will systematically vary the DNAs used as standards, utilizing standards of different sizes, and measure their relative fluorescence intensities. If necessary, empirical

correction factors are calculated to ensure linearity.

DEPP:
Optical Mapping of Large Mammalian Genomes: Ferrin and Camerini-Otero (68) have shown that two RARE sites can be designed to selectively cleave a sizable mammalian genomic stretch; it can then be resolved on a pulsed field gel from uncut genomic DNA. These authors, as well as Hook and Szybalski (67), suggested that these dissected and isolated genomic sections could be used to construct locus-specific libraries for physical mapping studies. These libraries help in tying contigs together or in mapping uncloneable regions, for example. Although directly mapping the small amount of cleaved, genomic DNA obtained from gels would be convenient, obviating steps and artifacts of cloning, the concentration of the recovered DNA is generally insufficient for direct analysis, except by PCR and optical mapping.

DEPR:
Influence of coil relaxation on detection of cuts. Aside from cases involving small fragments, incomplete digestion is seen in all the histograms in FIG. 7. While potential cases range from photo irradiation artifacts to interactions imposed by the current design of the microscope chamber, partial digestion observed here is attributable mostly to incomplete coil relaxation at a given cut site, due to relaxation modes that fail to produce a gap or distinct ball. A variety of different relaxation modes are observed in actual practice, some of which are sketched in FIG. 8. Relaxation modes can both facilitate (8-D) and hinder cut detection (8-H). Application of electric or flow fields might be used to trigger relaxation at such sites and permit their detection. Parallel electrophoresis experiments show essentially complete digestion under similar experimental conditions (Hernandez).

CCOR:
435/6

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☐ 1. Document ID: US 6143502 A

L2: Entry 1 of 6 File: USPT Nov 7, 2000

US-PAT-NO: 6143502
DOCUMENT-IDENTIFIER: US 6143502 A

TITLE: Dual-luciferase reporter system

DATE-ISSUED: November 7, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Grentzmann; Guido	Salt Lake City	UT	N/A	N/A
Gesteland; Raymond F.	Salt Lake City	UT	N/A	N/A
Atkins; John F.	Verrieres le Buisson	N/A	N/A	FRX

US-CL-CURRENT: 435/6; 435/320.1, 435/8

ABSTRACT:

Plasmids and methods of use for assaying translational recoding are disclosed. The plasmids contain a constitutively expressed renilla (Renilla reniformis; sea pansy) luciferase gene, a polylinker for insertion of a selected DNA segment, and an out-of-frame firefly luciferase gene. Recoding is determined by monitoring luminescence of the firefly luciferase normalized to the luminescence of the renilla luciferase.

26 Claims, 4 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 2. Document ID: US 6110671 A

L2: Entry 2 of 6 File: USPT Aug 29, 2000

US-PAT-NO: 5,811,671
DOCUMENT-IDENTIFIER: US 5811671 A

TITLE: Method of measuring tumor suppressor gene p53

DATE-ISSUED: August 29, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kim; Jerome H.	Baltimore	MD	N/A	N/A

US-CL-CURRENT: 435/6; 435/91.2, 536/23.1, 536/24.3, 536/24.32, 536/24.33

ABSTRACT:

The instant invention provides a means for quantitatively determining the vel of tumor suppressor gene p53 by determination of level of messenger ribonucleic acid (mRNA) of the gene in a sample when compared with a prepared standard. The assay is quantitative in that the specific number of copies of the p53 mRNA in a sample may be derived from a curve from a standard of p53 RNA. The RNA used in preparation of a standard curve to quantitate RNA is generated using a plasmid which is part of the invention. In the assay, the RNA is produced by a protein (RNA polymerase) that reads the DNA message and manufactures an RNA copy. The RNA content of the transcribed sample is determined spectrophotometrically to measure the molar concentration. With prior knowledge of the molecular weight of the transcribed RNA and using Avogadro's number, the actual number of molecules of transcripted "control" p53 RNA can be determined

4 Claims, 0 Drawing figures Exemplary Claim Number: 1

☐ 3. Document ID: US 5677133 A

L2: Entry 3 of 6 File: USPT Oct 14, 1997

US-PAT-NO: 5677133
DOCUMENT-IDENTIFIER: US 5677133 A

TITLE: Dry chemistry cascade immunoassay and affinity assay

DATE-ISSUED: October 14, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Oberhardt; Bruce J.	Raleigh	NC	N/A	N/A

US-CL-CURRENT: 435/7.1; 422/57, 422/58, 422/61, 422/73, 435/13, 435/288.5, 435/288.7, 436/5, 435/6, 435/7.2, 435/7.4, 435/7.7, 435/7.92, 435/7.93, 435/7.94, 435/810, 436/46, 436/526, 436/527, 436/805, 436/806, 436/807, 436/808, 436/809, 436/810

ABSTRACT:

A method is described for performing an affinity assay comprising contacting a sample to be assayed for the presence of an analyte with a dry reagent containing the analyte (hapten, antigen, antibody, receptor, or complementary polynucleotide) bound to a reaction cascade initiator, an antibody or other binding pair partner reactive with said analyte, and magnetic particles, to form an assay mixture in a reaction chamber, incubating the assay mixture, applying an oscillating or moving static magnetic field to the assay mixture, activating the reaction cascade initiator to initiate a reaction cascade, monitoring the response of the magnetic particles to the oscillating or moving static magnetic field to provide a time varying signal, and determining the analyte concentration of the sample by analysis of the time varying signal, as well as a kit for performing the assay and a diagnostic system for performing the assay.

4 Claims, 20 Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 10

☐ 4. Document ID: US 5601991 A

L2: Entry 4 of 6 File: USPT Feb 11, 1997

US-PAT-NO: 5621991
DOCUMENT-IDENTIFIER: US 5621991 A

TITLE: Dry chemistry cascade immunoassay and affinity assay

DATE-ISSUED: February 11, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Eberhardt; Bruce J.	Raleigh	NC	N/A	N/A

US-CL-CURRENT: 435/7.91; 422/57, 422/58, 422/61, 422/73, 435/13, 435/5, 435/6, 435/7.2, 435/7.4, 435/7.7, 435/7.92, 435/7.93, 435/7.94, 435/808, 435/810, 435/973, 436/46, 436/526, 436/527, 436/805, 436/806, 436/807, 436/809, 436/809

ABSTRACT:

A method is described for performing an affinity assay comprising contacting a sample to be assayed for the presence of an analyte with a dry reagent containing the analyte (hapten, antigen, antibody, receptor, or complementary polynucleotide) bound to a reaction cascade initiator, an antibody or other binding pair partner reactive with said analyte, and magnetic particles, to form an assay mixture in a reaction chamber, incubating the assay mixture, applying an oscillating or moving static magnetic field to the assay mixture, activating the reaction cascade initiator to initiate a reaction cascade, monitoring the response of the magnetic particles to the oscillating or moving static magnetic field to provide a time varying signal, and determining the analyte concentration of the sample by analysis of the time varying signal, as well as a kit for performing the assay and a diagnostic system for performing the assay.

86 Claims, 2. Drawing figures Exemplary Claim Number: 1
Number of Drawing Sheets: 10

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

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☐ 5. Document ID: US 5225332 A

L2: Entry 5 of 6 File: USPT Jul 6, 1993

US-PAT-NO: 5225332
DOCUMENT-IDENTIFIER: US 5225332 A

TITLE: Process for manipulation of non-aqueous surrounded microdroplets

DATE ISSUED: July 6, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weaver; James C.	Sudbury	MA	N/A	N/A
Joseph; Julian	Cedarhurst	NY	N/A	N/A

US-CL-CURRENT: 435/29; 428/402.2, 435/177, 435/182, 435/243, 435/30, 435/34, 435/5, 435/6, 435/7.1, 436/526, 436/535, 436/829

ABSTRACT:

A process for manipulation of liquid microdroplets is disclosed. The process involves formation of microdroplets such that physical forces based on particular interactions of the microdroplets with a surrounding non-aqueous fluid results can be used to alter the position of the microdroplets.

7 Claims, 0 Drawing figures Exemplary Claim Number: 1,4,5

☐ 6. Document ID: US 4959301 A

L2: Entry 6 of 6 File: USPT Sep 25, 1990

US PAT-NO: 4959301
DOCUMENT-IDENTIFIER: US 4959301 A

TITLE: Process for rapidly enumerating viable entities

DATE-ISSUED: September 25, 1990

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weaver; James C.	Sudbury	MA	N/A	N/A
Bliss; Jonathan G.	Somerville	MA	N/A	N/A
Williams; Gregory B.	Tewksbury	MA	N/A	N/A
Powell; Kevin T.	Boston	MA	N/A	N/A
Harrison; Gail I.	Watertown	MA	N/A	N/A

US-CL-CURRENT: 435/5; 435/177, 435/182, 435/29, 435/30, 435/32, 435/39, 435/6

ABSTRACT:

A process for rapidly enumerating viable biological entities is disclosed, wherein viability is determined by the critierion of growth of biological entities contained in microdroplets. Alternatively, in some cases, viability is determined by use of vital staining of biological entities contained in microdroplets. The process involves formation of microdroplets, which are very small volume liquid or gel particles, such that some of the microdroplets contain biological entities, followed by measurements of biological entities and of microdroplet volumes, such that use of statistical analysis can be used self-consistently to determine the number of viable entities per volume of a sample.

12 Claims, 9 Drawing figures Exemplary Claim Number: 1

WEST

Generate Collection

L2: Entry 1 of 6 File: USPT Nov 7, 2000

DOCUMENT-IDENTIFIER: US 6143502 A
TITLE: Dual-luciferase reporter system

DEPR:
The dual-luciferase assay is designed such that synthesis of the second reporter (firefly luciferase) is dependent on recoding. On its own, however, the amount of this reporter is not a direct reflection of the efficiency of recoding. In the absence of in-frame stop codons, a significant proportion of translating ribosomes disengage prematurely from the mRNA; this is often known as ribosome drop off. Early results from several laboratories have shown that 50% or more of Escherichia coli ribosomes drop off during synthesis of .beta.-galactosidase (J. L. Manley, Synthesis and Degradation of Termination and Premature-Termination Fragments of .beta.-Galactosidase In Vitro and In Vivo, 125 J. Mol. Biol. 407-432 (1979); C. G. Kurland et al., Limitations of Translational Accuracy, in F. C. Neidhardt et al., Escherichia coli and Salmonella typhimurium. Cellular and Molecular Biology 979-1004 (2.sup.nd ed. 1996)). Ribosomes that drop off while decoding the firefly reporter will lead to an underestimate of the proportion of ribosomes that respond to the recoding signals unless a correction is made. The basis for a correction factor is the assumption that drop off during synthesis of the firefly reporter is proportional to completion of synthesis of this reporter. The correction factor is provided by a control in which all ribosomes that complete synthesis of the first reporter (renilla luciferase) continue translation by starting synthesis of the firefly luciferase reporter.

CCOR:
435/6

WEST

Generate Collection

L2: Entry 2 of 6 File: USPT Aug 29, 2000

DOCUMENT-IDENTIFIER: US 6110671 A
TITLE: Method of measuring tumor suppressor gene p53

BSPR:
The .beta.-actin curves are used to standardize the p53 copy number. For example, the p53 assay is performed using 2000 "cell equivalents of RNA determined from the number of cells counted by means such as hemocytometer. The p53 number control curve is calculated as used to estimate the number of copies of p53 found in a sample of 2000 cells. The separate RT-PCR for .beta.-actin can be performed on 500 cell equivalents of RNA from the sample and then compared to the data obtained from a serial dilution (100 cell equivalents to 1 cell equivalent) of RNA from a control PBMC sample. From this comparison a correction factor is obtained. For example, the .beta.-actin data may suggest that there is only 100 cell equivalents of RNA in the sample tested rather than the 500 cell equivalents expected under the circumstances. The p53 copy number of that sample is multiplied by a factor of 5 to correct for the "deficiency" in cell number.

DCOR:
435/6

WEST

Generate Collection

L2: Entry 3 of 6 File: USPT Oct 14, 1997

DOCUMENT-IDENTIFIER: US 5677193 A
TITLE: Dry chemistry cascade immunoassay and affinity assay

DEPR:
To perform the quinidine assay, the reaction slide is placed in the instrument and automatically brought to operating temperature, typically 37.degree. C. for this assay system. A drop of blood is added to the reaction slide and sample well. The blood enters and dissolves the reagent. The magnetic particles are driven into motion by application of an oscillating magnetic field creating convection and mixing the reactants. During this period the anti-quinidine antibody is allowed to bind to the quinidine on the X.sub.a mutant-quinidine conjugate and to quinidine that may be present in the sample. This distribution of the fixed amount of antibody between conjugate and sample quinidine occurs as the reaction is allowed to continue during a predetermined incubation period. At the end of this incubation period, the temperature set point is rapidly increased by 8.degree. C./min to a level at which the X.sub.a mutant undergoes a conformational change and becomes active. At this point, the X.sub.a enzyme begins to convert prothrombin to thrombin at a rate proportional to the concentration of active X.sub.a enzyme. The X.sub.a enzyme sterically inactivated by antibody does not convert prothrombin to thrombin or converts it at an extremely low or negligible rate. Therefore, the concentration of X.sub.a -quinidine conjugate that has not reacted with antibody determines the rate of conversion of prothrombin to thrombin. The generated thrombin converts fibrinogen to fibrin, thus amplifying the chemical signal further. When fibrin formation reaches a critical stage, the clot or endpoint is detected by changes in the magnetic particle movement. The elapsed time from thermal triggering to clot endpoint is the clotting time. The clotting time is thus proportional to the quinidine in the sample. The actual quinidine concentration in the sample can be read automatically from a standard curve stored in the measuring instrument for that particular lot of reaction slides. This value can be converted to a plasma quinidine concentration, if desired, by correcting for the fraction of the reaction volume occupied by blood cells. A correction factor for total cell volume, in blood typically equivalent to hematocrit, may be entered into the instruments computer memory or this conversion may be performed from a simple chart.

CCXR:
435/6

WEST

End of Result Set

Generate Collection

L2: Entry 6 of 6 File: USPT Sep 25, 1990

DOCUMENT-IDENTIFIER: US 4959301 A
TITLE: Process for rapidly enumerating viable entities

DEPL:
which is the intermediate of the assay, thereby being the number of analyte entities per volume in the diluted sample. It is straightforward to then compute a correction factor, .function..sub.D, ##EQU16## for the dilution during the MD creation process, and thereby, to obtain the concentration, .rho..sub.analyte, of analyte entity in the (original) sample.

CCXR:
435/6

WEST

Generate Collection

L2: Entry 5 of 6 File: USPT Jul 6, 1993

DOCUMENT IDENTIFIER: US 5225332 A
TITLE: Process for manipulation of non-aqueous surrounded microdroplets

DEPR:
The number of MD groups found by measurement of fluorescence of individual MD groups to contain n=2, n=3, etc. enzyme labeled specific binding molecules is then used to compute a best value of n for each range (interval) of V.sub.group values, and then to compute the best value of .rho. by applying the equation ##EQU17## which is the intermediate of the assay, thereby being the number of analyte entities per volume in the diluted sample. It is straightforward to then compute a correction factor, f.sub.D, ##EQU18## for the dilution during the MD creation process, and thereby, to obtain the concentration, .rho..sub.analyte, of analyte entity in the (original) sample.

CCXR:
435/6

L2 ANSWER 12 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 6
AN 1997:366491 BIOSIS
DN PREV199799859424
TI Visual pigment gene structure and expression in human retinae.
AU Yamaguchi, Tomohiko; Motulsky, Arno G.; Deeb, Samir S. (1)
CS (1) Dep. Med., Univ. Washington, Seattle, WA 98195 USA
SO Human Molecular Genetics, (1997) Vol. 6, No. 7, pp. 981-990.
ISSN: 0964-6906.
DT Article
LA English
AB We determined the genotypes of the X-chromosome-linked red/green color

WEST

End of Result Set

Generate Collection

L4: Entry 1 of 1 File: USPT Dec 22, 1998

DOCUMENT-IDENTIFIER: US 5851760 A
TITLE: Method for generation of sequence sampled maps of complex genomes

DEPR:
It was found that the prehybridization of the RNA probes with a high concentration of human repetitive sequences, as hereinabove described, was sufficient to completely block hybridization of most of these frequencies, and was sufficient for eliminating most of these artifactual linkages. However, the analysis of several large contigs mapping to human chromosome 11 generated by this analysis has revealed several cosmid clones which were included in a contig but which could not be substantiated based on the result of restriction mapping and hybridization analysis. This artifact may be the result of cryptic low-frequency repetitive or redundant sequences present in this region of the genome, or could be the result of genomic sequences which are unstable and deleted or rearrange when cloned in E. coli. Evidence for the later sequences, isolated through screening non-amplified cosmid libraries, has been found in the analysis of the human CD3 locus [Evans et al., Immunogen, Supra]. However, it should be noted that the multiplex technique of the present invention, when carried to completion using both T3 and T7 mixed RNA probes, generates data that is internally redundant in that both members of a linked pair should cross-hybridize with one another. Thus, further refinement of this approach should eliminate most serious artifacts arising during multiplex clone analysis.

CCOR:
435/6

ORPL:
Lichter, et al., "Rapid Detection Of Human Chromosome 21 Abberations By in situ Hybridization," Proc. Natl. Acad. Sci.(USA), 85:9664-9668 (1988).

correction before date

Trying 31.[illegible]...Open

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NEWS 5	Oct 27	Patent Assignee Code Dictionary now available in Derwent Patent Files
NEWS 6	Oct 27	Plasdoc Key Serials Dictionary and Echoing added to Derwent Subscriber Files WPIDS and WPIX
NEWS 7	Nov 29	Derwent announces further increase in updates for DWPI
NEWS 8	Dec 5	French Multi-Disciplinary Database PASCAL Now on STN
NEWS 9	Dec 5	Trademarks on STN - New DEMAS and EUMAS Files
NEWS 10	Dec 15	2001 STN Pricing
NEWS 11	Dec 17	Merged CEABA-VTB for chemical engineering and biotechnology
NEWS 12	Dec 17	Corrosion Abstracts on STN
NEWS 13	Dec 17	SYNTHLINE from Prous Science now available on STN
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=> s (filter or artifact or anomali) and (gene (array or chip))

MISSING OPERATOR 'GENE (ARRAY'
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=> s (filter or artifact or anomali) and (gene w (array or chip))

MISSING OPERATOR 'W (ARRAY'
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nested terms that are not separated by a logical operator.

=> s (filter or artifact or anomali) and (gene adj (array or chip))

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)

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PROCESSING COMPLETED FOR L1
L2   17 DUP REM L1 (21 DUPLICATES REMOVED)

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L2   ANSWER 1 OF 17 CAPLUS COPYRIGHT 2001 ACS
AN   2001:44429 CAPLUS
TI   Number and Variations of the Red and Green Visual Pigment Genes in
     Japanese Men with Normal Color Vision
AU   Hayashi, S.; Ueyama, H.; Tanabe, S.; Yamade, S.; Kani, K.
CS   Otsu, Japan
SO   Jpn. J. Ophthalmol. (2001), 45(1), 60-67
     CODEN: JJOPA7; ISSN: 0021-5155
PB   Elsevier Science Inc.
DT   Journal
LA   English
AB   Purpose: We analyzed the red/green visual pigment genes in color-normal
     Japanese men to understand the relationship between color
     anomalies and genetic defects.Methods: DNA from 120 color-normal
     Japanese men was subjected to polymerase chain reaction
     (PCR)-amplification for exons 2-5 of the red/green visual pigment genes
     and the PCR products were sequenced. The red:green gene ratios were estd.
     from the sequencing electropherograms of exon 5 and also from
     MvaI-restriction fragment anal. of the same exon. The first gene and the
     downstream genes in the pigment **gene array** were sep.
     analyzed by PCR, direct sequencing, and/or single-strand conformation
     polymorphisms.Results: The red:green gene ratios estd. from the ratios of
     peak heights of nucleotides on the sequencing electropherograms coincided
     with those estd. from the MvaI-restriction fragment anal. Among the
     subjects analyzed, they were 1:1 in 43 (n = 52), 1:2 in 41 (n = 49), 1:3
     in 6 (n = 7), and 1:>3 in 9 (n = 11). The first gene in the pigment
     gene arrays was red in all subjects. Only 1 subject
     NA22 had a green-red hybrid gene. Exons 2 and 4 had 2 haplotypes each,
     but exon 3 was highly polymorphic. Exon 5 of the green genes had one
     polymorphism at codon 233 with a frequency of 32 .Conclusions: The
     features of visual pigment genes in color-normal Japanese men were

revealed. The data and establishing techniques may be useful for analyzing these genes in color-deficient subjects in the Japanese population.

L2 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2001 ACS
AN 2000:911156 CAPLUS
DN 134:52249
TI System for eliminating background in **gene chip** array analysis
IN Bliton, Allison C.
PA Genomic Solutions Inc., USA
SO PCT Int. Appl., 9 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000077250	A1	20001218	WO 2000-US16696	20000616

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-140063 19990618
US 2000-596332 20000616
AB A system to eliminate background in optically scanned samples is disclosed which selectively blocks excitation or emission light through the use of **filters**.
RE.CNT 3
RE
(1) Hoyt; US 5143129 A 1992 CAPLUS
(2) Sampas; US 5930943 A 1999
(3) Trost; US 6066245 A 2000 CAPLUS

L2 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 1
AN 2000:856693 CAPLUS
TI A pulmonary rat **gene array** for screening altered expression profiles in air pollutant-induced lung injury
AU Nadadur, Srikanth S.; Schladweiler, Mette C. J.; Kodavanti, Urmila P.
CS Curriculum in Toxicology, University of North Carolina, Chapel Hill, NC, 27711, USA
SO Inhalation Toxicol. (2000), 12(12), 1239-1254
CODEN: INHTE5; ISSN: 0895-8378
PB Taylor & Francis
DT Journal
LA English
AB Pulmonary tissue injury and repair processes involve complex and coordinated cellular events such as necrosis, inflammation, cell growth/differentiation, apoptosis, and remodeling of extracellular matrix. These processes are regulated by expression of multiple mediator genes. Com. available microarray blots and slides allow screening of hundreds to thousands of genes in a given tissue or cell prepn. However, often these blots do not contain cDNAs of one's interest and are difficult to interpret. In order to analyze the tissue expression profile of a large no. of genes involved in pulmonary injury and pathol., we developed a rat **gene array filter** using array technol. This array consisted of 27 genes representing inflammatory and anti-inflammatory cytokines, growth factors, adhesion mols., stress proteins, transcription factors and antioxidant enzymes; 3 neg. controls, and 2 blank spots. Using rat gene-specific polymerase chain reaction (PCR) primer pairs, cDNAs for these genes were amplified and cloned into a TA vector. Plasmids with recombinant cDNA inserts were purified and blotted onto a nylon membrane. Lung total RNA was isolated at 3 or 24 h following intratracheal (IT) exposure of male Sprague Dawley rats to

either saline (control), residual oil fly ash (ROFA; 8.[illegible]g/kg), or metals found in one instillate of ROFA: nickel ($NiSO_4$; 1.3 .mu.mol/kg), or vanadium (VSO_4; 1.2 .mu.mol/kg). ^{32}P-Labeled cDNA was generated from RNA samples.

RE.CNT 25

RE

(1) Barnes, P; Eur Respir J 1998, V12, P221 CAPLUS
(2) Bittner, M; Nat Genet 1999, V22, P213 CAPLUS
(4) DeRisi, J; Nat Genet 1996, V14, P457 CAPLUS
(6) Dreher, K; J Toxicol Environ Health 1997, V50, P285 CAPLUS
(8) Hatch, G; Environ Res 1985, V36, P67 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 17 SCISEARCH COPYRIGHT 2001 ISI (R)
AN 2000:671548 SCISEARCH
GA The Genuine Article (R) Number: 347EF
TI Fundamentals of DNA hybridization arrays for gene expression analysis
AU Freeman W M; Robertson D J; Vrana K E (Reprint)
CS WAKE FOREST UNIV, SCH MED, DEPT PHYSIOL & PHARMACOL, MED CTR BLVD, WINSTON SALEM, NC 27157 (Reprint); WAKE FOREST UNIV, SCH MED, DEPT PHYSIOL & PHARMACOL, WINSTON SALEM, NC 27157
CYA USA
SO BIOTECHNIQUES, NOV 2000, Vol. 29, No. 5, pp. 1042-&.
Publisher: EATON PUBLISHING CO, 154 E. CENTRAL ST, NATICK, MA 01760.
ISSN: 0736-6205.
DT General Review; Journal
FS LIFE
LA English
REC Reference Count: 59
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB DNA hybridization arrays [also known as macroarrays, microarrays and/or high-density oligonucleotide arrays (**Gene Chips**(TM))] bring gene expression analysis to a genomic scale by permitting investigators to simultaneously examine changes in the expression of literally thousands of genes. For hybridization arrays, the general approach is to immobilize gene-specific sequences (probes) on a solid state matrix (nylon membranes, glass microscope slides, silicon/ceramic chips). These sequences are then queried with labeled copies of nucleic acids from biological samples (targets). The underlying theory is that the greater the expression of a gene, the greater the amount of labeled target, and hence, the greater output signal. In spite of the simplicity of the experimental design, there are at least four different platforms and several different approaches to processing and labeling the biological samples. Moreover, investigators must also determine whether they will utilize commercially available arrays or generate their own. This review will cover the status of the hybridization array field with an eye toward underlying principles and available technologies. Further developments and technological trends will also be evaluated.

L2 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2001 ACS DUPLICATE 2
AN 2000:883502 CAPLUS
TI Correlation of Gene Structure and Psychophysical Measurement in Red-Green Color Vision Deficiency in Chinese
AU Zhang, Q.; Xiao, X.; Shen, H.; Li, S.; Jiang, F.
CS National Ophthalmological Labs and Zhongshan Ophthalmic Center, Ocular Genetics and Molecular Biology, Sun Yat-Sen University of Medical Sciences, Canton, Peop. Rep. China
SO Jpn. J. Ophthalmol. (2000), 44(6), 596-600
CODEN: JJOPA7; ISSN: 0021-5155
PB Elsevier Science Inc.
DT Journal
LA English
AB Purpose: To study the correlation of genotype for X-linked red-green **gene array** with color vision phenotype in 58 subjects with red-green color vision deficiency.Methods: The mol. structure of red and green pigment genes on 58 X chromosomes was studied exon-by-exon by using heteroduplex-SSCP anal. and sequencing. The color vision of these subjects was detd. by a Neitz **anomaloscope**.Results: Variations in the red and green pigment genes were detected in 43 subjects and a

hybrid gene was found [redacted]27 subjects. About 5[illegible] of the [redacted]sion sites occurred at intron 2-3[illegible] All 3 **anomalous** trichromats wi[illegible] intron 4 fusion were mild type but another 1 with intron 2-3 fusion were severe type. No subjects with mild type of color vision defects had a fusion site at intron 2-3 or its upstream. Three subjects with complete deletion of the green pigment gene manifested deuteranomaly.Conclusions: Protans can be differentiated from deutans on the basis of genotype. It is still difficult to establish a clear correlation of different **anomalous** trichromats with genotype. The fusion site of a hybrid gene affects the phenotype to some degree. Intron 2-3 is the common place for gene crossover.

RE.CNT 12

RE

(1) Asenjo, A; Neuron 1994, V12, P1131 CAPLUS

(3) Deeb, S; Am J Hum Genet 1992, V51, P687 CAPLUS

(4) Hayashi, T; Nat Genet 1999, V22, P90 CAPLUS

(5) Nathans, J; Science 1986, V232, P193 CAPLUS

(6) Nathans, J; Science 1986, V232, P203 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 3

AN 1999:104047 BIOSIS

DN PREV199901104047

TI Direct visual resolution of gene copy number in the human photopigment **gene array**.

AU Wolf, Stephan; Sharpe, Lindsay T. (1); Schmidt, Hans-Juergen A.; Knau, Holger; Weltz, Sandra; Kroeschis, Petra; Poustka, Annemarie; Brenner, Eberhart; Lichter, Peter; Wissinger, Bernd

CS (1) Forschungsstelle fuer Experimentelle Ophthalmologie, Universitaets-Augenklinik, Roentgenweg 11, D-72076, Tuebingen, Germany

SO IOVS, (June, 1999) Vol. 40, No. 7, pp. 1585-1589.

DT Article

LA English

SL English

AB PURPOSE. To visualize by direct fluorescent in situ hybridization the entire human visual pigment **gene array** in single X-chromosome fibers and to compare the results with values obtained by other molecular techniques. METHODS. The size of the opsin **gene array** on the X-chromosome in eight male subjects was investigated by (i) direct visual in situ hybridization (DIRVISH) on elongated DNA fibers; (ii) quantitation of genomic restriction fragments after Southern blot hybridization; (iii) quantitation of restriction fragment length polymorphism after PCR amplification (PCR/RFLP); and (iv) sizing of NotI fragments by pulsed field gel electrophoresis and Southern blot detection. Each male subject's color vision was assessed by Rayleigh matches on a Nagel Type I **anomaloscope**. RESULTS. The number of genes resolved by the DIRVISH protocol, which ranges from 1 to 6, agrees exactly with the **gene array** sizes obtained in the same male subjects from pulsed field gel electrophoresis, but differs from the estimates derived from the commonly used indirect Southern blot hybridization and PCR/RFLP quantitation methods. In particular, the PCR/RFLP method overestimates the copy number in all but the smallest arrays. CONCLUSIONS. Visualization of the X-chromosome opsin **gene array** by DIRVISH provides a new, direct method for obtaining exact copy numbers and helps to resolve the controversy about the range and the average visual pigment gene number in the human population in favor of smaller average array sizes.

L2 ANSWER 7 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2000:143951 BIOSIS

DN PREV200000143951

TI Analysis of gene expression following traumatic brain injury using gene expression array technology.

AU Harrison, S. M. W. (1); Davis, B. M. (1); Sullivan, P. G. (1); Scheff, S. W. (1

CS (1) Dept. of Anatomy and Neurobiology, University of Kentucky College of Medicine, Lexington, KY, 40536 USA

SO Society for Neuroscience Abstracts., (1999) Vol. 25, No. 1-2, pp. 82.. Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999 Society for Neuroscience

. ISSN: 0193-5295.
DT Conference
LA English
SL English

L2 ANSWER 9 OF 17 SCISEARCH COPYRIGHT 2001 ISI (R)
AN 1999:917517 SCISEARCH
GA The Genuine Article (R) Number: 258MM
TI Application of DNA arrays to toxicology
AU Rockett J C (Reprint); Dix D J
CS US EPA, NATL HLTH & ENVIRONM EFFECTS RES LAB, REPRODUCT TOXICOL DIV MD72, RES TRIANGLE PK, NC 27711 (Reprint)
CYA USA
SO ENVIRONMENTAL HEALTH PERSPECTIVES, (AUG 1999) Vol. 107, No. 8, pp. 681-685.
Publisher: US DEPT HEALTH HUMAN SCIENCES PUBLIC HEALTH SCIENCE, NATL INST HEALTH, NATL INST ENVIRONMENTAL HEALTH SCIENCES, PO BOX 12233, RES TRIANGLE PK, NC 27709-2233.
ISSN: 0091-6765.
DT Article; Journal
FS LIFE; AGRI
LA English
REC Reference Count: 14
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB DNA array technology makes it possible to rapidly genotype individuals or quantify the expression of thousands of genes on a single **filter** or glass slide, and holds enormous potential in toxicologic applications. This potential led to a U.S. Environmental Protection Agency-sponsored workshop titled ''Application of Microarrays to Toxicology'' on 7-8 January 1999 in Research Triangle Park, North Carolina. In addition to providing state-of-the-art information on the application of DNA or gene microarrays, the workshop catalyzed the formation of several collaborations, committees, and user's groups throughout the Research Triangle Park area and beyond. Potential application of microarrays to toxicologic research and risk assessment include genome-wide expression analyses to identify gene-expression networks and toxicant-specific signatures that can be used to define mode of action, for exposure assessment, and for environmental monitoring. Arrays may also prove useful for monitoring genetic variability and its relationship to toxicant susceptibility in human populations.

L2 ANSWER 9 OF 17 CAPLUS COPYRIGHT 2001 ACS
AN 1998:672693 CAPLUS
DN 129:272647
TI Biomolecular processor for isolation and purifn. of nucleic acids
IN Fields, Robert E.
PA USA
SO PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9842874	A2	19981001	WO 1998-US6029	19980323
	WO 9842874	A3	19981223		
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9867790	A1	19981020	AU 1998-67790	19980323
	EP 972080	A2	20000119	EP 1998-913175	19980323
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	US 1997-41237		19970324		

WO 1999-US[illegible] 1999[illegible]

AB A process and app. are described for isolating and purifying nucleic acids and other target mols. directly from blood, plasma, urine, cell cultures and the like by totally automated means, without centrifugation, aspiration or vacuum. After mixing and heating a nucleic acid contg. sample with lysis reagent in an environmentally isolated compartment, nucleic acids are absorbed onto a binding **filter** and eluted in a small vol. using heated elution reagent. A preferred embodiment purifies nucleic acids and automatically detects target sequences from a sample of fresh blood. Another embodiment purifies target mols. from a multitude of samples held in multiwell plates. Test kits for each embodiment include disposable isolation and detection devices and associd. reagents.

L2 ANSWER 10 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 4
AN 1999:39417 BIOSIS
DN PREV199900039417
TI Red, green, and red-green hybrid pigments in the human retina: Correlations between deduced protein sequences and psychophysically measured spectral sensitivities.
AU Sharpe, Lindsay T. (1); Stockman, Andrew; Jagle, Herbert; Knau, Holger; Klausen, Gert; Reitner, Andreas; Nathans, Jeremy
CS (1) Forschungsstelle Exp. Opthalmol., Univ.-Augenklin. Abteilung II, D-72076 Tuebingen Germany
SO Journal of Neuroscience, Dec. 1, 1998 Vol. 18, No. 23, pp. 10053-10069. ISSN: 0270-6474.
DT Article
LA English
AB To analyze the human red, green, and red-green hybrid cone pigments in vivo, we studied 41 male dichromats, each of whose X chromosome carries only a single visual pigment gene (single-gene dichromats). This simplified arrangement avoids the difficulties of complex plain **gene arrays** and overlapping cone spectral sensitivities present in trichromats and of multiple genes encoding identical or nearly identical cone pigments in many dichromats. It thus allows for a straightforward correlation between each observer's spectral sensitivity measured at the cornea and the amino acid sequence of his visual pigment. For each of the 41 single gene dichromats we determined the amino acid sequences of the X-linked cone pigment as deduced from its gene sequence. To correlate these sequences with spectral sensitivities in vivo, we determined the Rayleigh matches to different red/green ratios for 23 single-gene dichromats and measured psychophysically the spectral sensitivity of the remaining green (middle wavelength) or red gene (long wavelength) genes in 37 single-gene dichromats. Cone spectral sensitivity maxima obtained from subjects with identical visual pigment amino acid sequences show up to a approx3 nm variation from subject to subject, presumably because of a combination of inexact or not corrections for variation in preretinal absorption, variation in photopigment optical density, optical effects within the photoreceptor, and measurement error. This variation implies that spectral sensitivities must be averaged over multiple subjects with the same genotype to obtain representative values for a given pigment. The principal results of this study are that (1) approx54% of the single-gene protanopes (and approx10% of all protanopes) possess any one of several 5'red-3'green hybrid genes that encode **anomalous** pigments and that would be predicted to produce protanomaly if present in **anomalous** trichromats; (2) the alanine/serine polymorphism at position 180 in the red pigment gene produces a spectral shift of approx2.7 nm; (3) for each exon the set of amino acids normally associated with the red pigment produces spectral shifts to longer wavelengths, and the set of amino acids normally associated with the green pigment produces spectral shifts to shorter wavelengths; and (4) changes in exons 2, 3, 4, and 5 from green to red are associated with average spectral shifts to long wavelengths of approx1 nm (range, -0.5 to 2.5 nm), approx3.3 nm (range, -0.8 to 7 nm), approx2.8 nm (range, -0.9 to 6 nm), and approx24.9 nm (range, 22.2-27.6 nm).

L2 ANSWER 11 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 5
AN 1999:148500 BIOSIS
DN PREV199900148500
TI Individual variations in color vision and its molecular biology.

AU Kitahara, Kenji (1)
CS (1) Dep. Ophthalmology, Jikei Univ. Sch. Med., 3-25-8 Nishi-shinbashi, Minato-ku, Tokyo 105-8461 Japan
SO Nippon Ganka Gakkai Zasshi, (Dec., 1998) Vol. 102, No. 12, pp. 837-849. ISSN: 0029-0203.
DT Article
LA Japanese
SL Japanese; English.
AB Individual variations in normal color vision and congenital red-green color vision defects in Japanese males were investigated using both psychophysics and molecular biology techniques. 1. Normal color vision. We studied 42 Japanese males who were diagnosed as having normal color vision using the Ishihara plates test and Nagel model I **anomaloscope**. The structure of the **gene arrays** of the X-linked L- and M-pigment genes was determined using quantitative PCR-SSCP (polymerase chain reaction-single strand conformation polymorphism). We found the following variations of the number of M-pigment genes: 27 (64%) of these men had only one M-pigment gene, 13 (31%) had two, 1 (2%) had three and 1 (2%) had four. Two common polymorphisms were found at amino acid residue 180 of both L- and M-opsin, of the total 56 (78%) were Ser and the other 16 (22%) were Ala in the L-pigment and of the total 65 (90%) were Ala and the other 7(10%) were Ser in the M-pigment. The Rayleigh match midpoints fell within the normal range, however there were two fairly distinct groups with consistent differences in each group. The mean values of the proportion of red in a mixture of red and green were 0.564 +- 0.026 (mean +- standard deviation). Correlation was found only between the Rayleigh match midpoint and the polymorphism at residue 180 of L-pigment. In order to estimate the variations of L/M cone ratio in the retinae the spectral sensitivities using heterochromatic flicker method were measured. Using the hypothesis that the luminosity function is proportional to the sum of L- and M-cone spectral sensitivity (k L (lambda) + M (lambda)), the constant k values were obtained. The k values for the subjects with Ser180 and Ala180 L-pigment were 1.89 +- 1.44 and 1.88 +- 1.02 respectively. Furthermore, in order to study the variation of information processing system, the spectral sensitivities for 1 degree, 200-ms test flash on a white background were measured. Using the hypothesis that the spectral sensitivity is proportional to the difference of L- and M-cone spectral sensitivity (L (lambda) - k' M (lambda)), the k' values were obtained. The k' values for the subjects with Ser180 and Ala180 L-pigment were 1.38+-0.36 and 1.42+-0.07 respectively. As a result, it was suggested that there are individual variations in both the L/M cone ratio and the color opponent system. 2. Congenital red-green color vision deficiencies. We studied the structure of the **gene arrays** of the X-linked L- and M-pigment genes and investigated the relationship between genotype and phenotype in 21 Japanese males comprising 4 protanopia, 6 protanomaly, 7 deuteranopia and 4 deuteranomaly. All of the protan subjects had 5' L-M fusion gene with/without the M gene. All of the deutan subjects had a normal L gene with/without 5' M-L fusion gene. Genotype agreed with phenotype in 8 of 10 protan subjects and 10 of 11 deutan subjects. Two of them were diagnosed as abnormal trichromatism in spite of having only one gene. One of them was diagnosed as dichromatism in spite of having two genes that encoded spectrally different pigments. As a result, it was felt that the diagnosis of dichromacy and abnormal trichromacy with an **anomaloscope** has limitations.

L2 ANSWER 12 OF 17 BIOSIS COPYRIGHT 2002 BIOSIS DUPLICATE 6
AN 1997:366491 BIOSIS
DN PREV199799658424
TI Visual pigment gene structure and expression in human retinae.
AU Yamaguchi, Tomohiko; Motulsky, Arno G.; Deeb, Samir S. (1)
CS (1) Dep. Med., Univ. Washington, Seattle, WA 98195 USA
SO Human Molecular Genetics, (1997) Vol. 6, No. 7, pp. 981-990. ISSN: 0964-6906.
DT Article
LA English
AB We determined the genotypes of the X-chromosome-linked red/green color vision genes by a novel PCR/SSCP-based method and assessed expression by mRNA analysis in retinae of 51 unselected post mortem eye specimens from Caucasian males of unknown color vision status. All individuals had a

single red long-wave pigment gene and one or more [redacted] average of two green (middle-wave) pigment genes. Four males had 5'green-red3' hybrid genes in addition to normal red and green pigment genes. These findings are consistent with earlier studies on human visual pigment gene structure using Southern blotting and with a recent study using pulsed-field electrophoresis. We interpret claims of much larger numbers of red, green and green-red hybrid genes to be technical **artifacts**. The ratio of expressed red to green pigment retinal mRNA varied widely (1-16) with a mode of 4) and was not correlated with that of red to green pigment genes. In one individual with a green-red hybrid gene in addition to normal red and green pigment genes, the normal red pigment gene and the hybrid gene were both expressed, but the normal green gene was not. This person presumably had deuteranomalous color genes. These two individuals presumably had normal color vision. We interpret the failure to express their vision. Two with green-red hybrid genes expressed the normal red and green pigment genes, but not the hybrid genes. These two individuals presumably had normal color vision. We interpret the failure the express their green-red hybrid genes to be caused by their location at a more distal position in the visual pigment **gene array**.

L2 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2001 ACS
AN 1997:161011 CAPLUS
TI Thermodynamics of duplex formation and mismatch discrimination on photolithographically synthesized oligonucleotide arrays.
AU Forman, Jonathan E.; Walton, Ian D.; Stern, David; Rava, Richard P.; Trulson, Mark O.
CS Affymetrix, Santa Clara, CA, 95051, USA
SO Book of Abstracts, 213th ACS National Meeting, San Francisco, April 13-17 (1997), COMP-382 Publisher: American Chemical Society, Washington, D. C. CODEN: 64AOAA
DT Conference; Meeting Abstract
LA English
AB Oligonucleotide probes immobilized on solid supports are finding increasingly widespread application in genetic anal. To address the fundamental kinetic and thermodn. aspects of these systems, we have investigated duplex formation between a 20 base oligonucleotide and 240 probe sequences ranging from 16 to 20 bases in length on an Affymetrix **Gene Chip** array. Multiple kinetic components are obsd. in the duplex assocn. and dissocn. kinetics of each probe sequence. The dominant kinetic component in the assocn. data is similar to predicted soln. kinetics, but slower components are obsd. as well. A distribution of dissocn. rate consts. differing by as much as two orders of magnitude is obsd. for a given probe sequence. Equil. melt curves likewise show multicomponent behavior, and melting temps. are consistently lower than those of corresponding soln.-phase species. The effects of probe length heterogeneity, probe surface d., and mass transport **artifacts** on the obsd. data will be discussed.

L2 ANSWER 14 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 7
AN 1998:462177 BIOSIS
DN PREV199800476477
TI Polymorphism in the number of genes encoding long-wavelength-sensitive cone pigments among males with normal color vision.
AU Neitz, Maureen; Neitz, Jay (1); Grishok, Alla
CS (1) Dep. Ophthalmol., Med. Coll. Wis., 8701 Watertown Plank Road, Milwaukee, WI 53226-0509 USA
SO Vision Research, (1998) Vol. 38, No. 17, pp. 2389-2407. ISSN: 0042-6989.
DT Article
LA English
AB Examination by direct DNA sequence analysis of the X-linked visual pigment genes in 27 males with normal color vision reveals that almost half have two or more different genes encoding a long-wavelength-sensitive cone pigment. This is counter to the conventional theory proposed from results of Southern hybridization studies that there is a single long-wave pigment gene per X-chromosome. Further, the sequences and consideration of the structure of the X-linked pigment **gene array** suggest that the majority of the observers (as many as 2/3) have hybrid (or fusion) genes like those that have been proposed to underlie color

anomaly. In some observers the long-wave hybrid genes contain a substantial amount of middle-wave sequence, e.g. five observers have hybrid long-wave genes that contain middle-wave sequences that include exon 4. Three of those five have the hybrid as their only long-wave gene, and thus have no other gene that could potentially encode a long-wave pigment. In these subjects, it is the hybrid gene that produces their normal long-wavelength-sensitive cone pigment. The high frequency of hybrid genes indicates that they are normal variant forms of the long-wave gene. Contrary to what is commonly believed, the introduction and the expression of hybrid genes is not sufficient to cause color vision defects.

L2 ANSWER 15 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 8
AN 1993:4393 BIOSIS
DN PREV199395[illegible]4393
TI Genotype-phenotype relationships in human red/green color-vision defects: Molecular and psychophysical studies.
AU Deeb, Samir S. (1); Lindsey, Delwin T.; Hibiya, Yuzo; Sanocki, Elizabeth; Winderickx, Joris; Teller, Davida Y.; Motulsky, Arno G.
CS (1) Dep. Genetics, SK-50, Univ. Wash., Seattle, Wash. 98195
SO American Journal of Human Genetics, (1992) Vol. 51, No. 4, pp. 687-700. ISSN: 0002-9297.
DT Article
LA English
AB The relationship between the molecular structure of the X-linked red and green visual pigment genes and color-vision phenotype as ascertained by **anomaloscopy** was studied in 64 color-defective males. The great majority of red-green defects were associated with either the deletion of the green-pigment gene or the formation of 5' red-green hybrid genes or 5' green-red hybrid genes. A rapid PCR-based method allowed detection of hybrid genes, including those undetectable by Southern blot analysis, as well as more precise localization of the fusion points in hybrid genes. Protan color-vision defects appeared always associated with 5' red-green hybrid genes. Carriers of single red-green hybrid genes with fusion in introns 1-4 were protanopes. However, carriers of hybrid genes with red-green fusions in introns 2, 3, or 4 in the presence of additional normal green genes manifested as either protanopes or protanomalous trichromats, with the majority being protanomalous. Deutan defects were associated with green-pigment gene deletions, with 5'green-red hybrid genes, or, rarely, with 5' green-red hybrid genes. Complete green-pigment gene deletions or green-red fusions in intron 1 were usually associated with deuteranopia, although we unexpectedly found three carriers of a single red-pigment gene without any green-pigment genes to be deuteranomalous trichromats. All but one of the other deuteranomalous subjects had green-red hybrid genes with intron 1, 2, 3, or 4 fusions, as well as several normal green-pigment genes. The one exception has a grossly normal **gene array**, presumably with a more subtle mutation. Amino acid differences in exon 5 largely determine whether a hybrid gene will be more redlike or more greenlike in phenotype. Various discrepancies as to severity (dimirmacy or trichromacy) remain unexplained but may arise because of variability of expression, postreceptoral variation, or both. When phenotypic color-vision defects exist, the kind of defect (protan or deutan) can be predicted by molecular analysis. Red-green hybrid genes are probably always associated with protan color-vision defects, while the presence of green-red hybrid genes may not always manifest phenotypically with color-vision defects. Four subjects who were found to have 5' green-red hybrid genes in addition to normal red- and green-pigment genes had normal color vision as determined by **anomaloscopy**. These were discovered among a group of 129 Caucasian males who had been recruited as volunteers for a vision study. We hypothesize that green-red hybrid genes in a more distal (3') position of a **gene array** that includes one or more normal green genes may not be expressed sufficiently to measurably affect color vision.

L2 ANSWER 16 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 9
AN 1989:191589 BIOSIS
DN BA87:91809
TI MOLECULAR PATTERNS OF X CHROMOSOME-LINKED COLOR VISION GENES AMONG 134 MEN OF EUROPEAN ANCESTRY.

AU DRUMMOND-BORG M; DEEB [redacted]; MOTULSKY A G
CS CENT. INHERITED DISEASES, UNIV. WASHINGTON, SEATTLE, WA[redacted]NGTON, 98195.
SO PROC NATL ACAD SCI U S A, (1989) 86 (2), 983-987.
CODEN: PNASA6. ISSN: 0027-8424.
FS BA; OLD
LA English
AB We used Southern blot hybridization to study X chromosome-linked color vision genes encoding the apoproteins of red and green visual pigments in 134 unselected Caucasian men. One hundred and thirteen individuals (84.3 %) had a normal arrangement of their color vision pigment genes. All had one red pigment gene; the number of green pigment genes ranged from one to five with a mode of two. The frequency of molecular genotypes indicative of normal color vision (84.3 %) was significantly lower than had been observed in previous studies of color vision phenotypes. Color vision defects can be due to deletions of red or green pigment genes or due to formation of hybrid genes comprising portions of both red and green pigment genes [Nathans, J., Piantanida, T. P., Eddy, R. L., Shows, T. B., & Hogness, D. S. (1986) Science 232, 203-210]. Characteristic **anomalous** patterns were seen in 15 (11.2 %) individuals: 7 (5.2 %) had patterns characteristic of deuteranomaly (mild defect in green color perception), 2 (1.5 %) had patterns characteristic of deuteranopia (severe defect in green color perception), and 6 (4.5 %) had protan patterns (the red perception defects protanomaly and protanopia cannot be differentiated by current molecular methods). Previously undescribed hybrid gene patterns consisting of both green and red pigment gene fragments in addition to normal red and green genes were observed in another 6 individuals (4.5%). Only 2 of these patterns were considered as deuteranomalous. Thus, DNA testing detected **anomalous** color vision pigment genes at a higher frequency than expected from phenotypic color vision tests. Some color vision **gene arrays** associated with hybrid genes are likely to mediate normal color vision.

L2 ANSWER 17 OF 17 BIOSIS COPYRIGHT © 01 BIOSIS DUPLICATE 10
AN 1989:[redacted]3731 BIOSIS
DN BA87:[redacted]3731
TI MOLECULAR BASIS OF ABNORMAL RED-GREEN COLOR VISION A FAMILY WITH THREE TYPES OF COLOR VISION DEFECTS.
AU DRUMMOND-BORG M; DEEB S; MOTULSKY A G
CS DIV. MED. GENETICS, FG-25, UNIV. WASH., SEATTLE, WASH. 98195.
SO AM J HUM GENET, (1989) 44 (5), 675-683.
CODEN: AJHGAG. ISSN: 0002-9297.
FS BA; OLD
LA English
AB The molecular nature of three different types of X-linked color-vision defects, protanomaly, deuteranomaly, and protanopia, in a large 3-generation family was determined. In the protanomalous and protanopic males the normal red pigment gene was replaced by a 5' red-3' green fusion gene. The protanomalous male had more red pigment DNA in his fusion gene than did the more severely affected protanopic individual. The deuteranomalous individual had four green pigment genes and 5' green-3' red fusion gene. These results extend those of Nathans et al., who proposed that most red-green color-vision defects arise as a result of unequal cross-over between the red and green pigment genes. The various data suggest that differences in severity of color-vision defects associated with fusion genes are caused by differences in crossover sites between the red and green pigment genes. Currently used molecular methodology is not sufficiently sensitive to define these fusion points accurately, and the specific color-vision defect within the deutan or protan class cannot be predicted. The DNA patterns for color-vision genes of female heterozygotes have not previously been described. Patterns of heterozygotes may not be distinguishable from those of normals. However, a definite assignment of the various color pigment **gene arrays** could be carried out by family study. Two compound heterozygotes for color-vision defects who tested as normal by **anomaloscopy** were found to carry abnormal fusion genes. In addition, a normal red pigment gene was present on one chromosome and at least one normal green pigment gene was present on the other. Thus, the presence of normal green and red pigment genes insured normal color vision. The presence of fusion genes did not grossly influence color

perception in these individuals. A third compound heterozygote had decreased luminosity for yellow in one yet only.

=> s (correction factor)

L3 12826 (CORRECTION FACTOR)

=> s l3 and (dna) and (gene or array or chip or assay)

L4 19 L3 AND (DNA) AND (GENE OR ARRAY OR CHIP OR ASSAY)

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L5 15 DUP REM L4 (4 DUPLICATES REMOVED)

=> d his

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FILE 'BIOSIS, CAPLUS, MEDLINE, SCISEARCH' ENTERED AT 16:19:14 ON 01 FEB 2001
L1 10 S (FILTER OR ARTIFACT OR ANOMAL? AND ((GENE ARRAY) OR (GENE CH
L2 7 DUP REM L1 (3 DUPLICATES REMOVED)
L3 12826 S (CORRECTION FACTOR)
L4 19 S L3 AND (DNA) AND (GENE OR ARRAY OR CHIP OR ASSAY)
L5 15 DUP REM L4 (4 DUPLICATES REMOVED)

=> s l5 not l2

L6 13 L5 NOT L2

=> d l6 bib ab 1-13

L6 ANSWER 1 OF 13 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:61283 BIOSIS
DN PREV200100061283
TI High-density microarray-mediated **gene** expression profiling of Escherichia coli.
AU Wei, Yan; Lee, Jian-Ming; Richmond, Craig; Blattner, Frederick R.; Rafalski, J. Antoni; LaRossa, Robert A. (1)
CS (1) Central Research and Development, Biochemical Science and Engineering, Experimental Station, DuPont Company, Wilmington, DE, 19880-0173: Robert.A.LaRossa@usa.dupont.com USA
SO Journal of Bacteriology, (January, 2001) Vol. 183, No. 2, pp. 545-556. print.
ISSN: 0021-9193.
DT Article
LA English
SL English
AB A nearly complete collection of 4,290 Escherichia coli open reading frames was amplified and arrayed in high density on glass slides. To exploit this reagent, conditions for RNA isolation from E. coli cells, cDNA production with attendant fluorescent dye incorporation, **DNA-DNA** hybridization, and hybrid quantitation have been established. A brief isopropyl-beta-D-thiogalactopyranoside (IPTG) treatment elevated lacZ, lacY, and lacA transcript content about 30-fold; in contrast, most other transcript titers remained unchanged. Distinct RNA expression patterns between E. coli cultures in the exponential and transitional phases of growth were catalogued, as were differences associated with culturing in minimal and rich media. The relative abundance of each transcript was estimated by using hybridization of a genomic **DNA**-derived, fluorescently labeled probe as a **correction factor**. This inventory provided a quantitative view of the steady-state level of each mRNA species. **Genes** the expression of which was detected by this method were enumerated, and results were compared with the current

understanding of E. coli physiology.

L6 ANSWER 2 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN [illegible] BIOSIS
DN PREV199900442304
TI Ionizing radiation and genetic risks X. The potential "disease phenotypes" of radiation induced genetic damage in humans: Perspectives from human molecular biology and radiation genetics.
AU Sankaranarayanan, K. (1)
CS (1) Department of Radiation Genetics and Chemical Mutagenesis, Sylvius Laboratories, MGC, Leiden University Medical Centre, Wassenaarseweg 72, 2333 AL, Leiden Netherlands
SO Mutation Research, (Aug. 1, 1999) Vol. 429, No. 1, pp. 45-83. ISSN: 0027-5107.
DT General Review
LA English
SL English
AB Estimates of genetic risks of radiation exposure of humans are traditionally expressed as expected increases in the frequencies of genetic diseases (single-**gene**, chromosomal and multifactorial) over and above those of naturally-occurring ones in the population. An important assumption in expressing risks in this manner is that gonadal radiation exposures can cause an increase in the frequency of mutations and that this would result in an increase in the frequency of genetic diseases under study. However, despite compelling evidence for radiation induced mutations in experimental systems, no increases in the frequencies of genetic diseases of concern or other adverse effects (i.e., those which are not formally classified as genetic diseases), have been found in human studies involving parents who have sustained radiation exposures. The known differences between spontaneous mutations that underlie naturally-occurring single-**gene** diseases and radiation-induced mutations studied in experimental systems now permit us to address and resolve these issues to some extent. The fact that spontaneous mutations (among which are point mutations and **DNA** deletions generally restricted to the **gene**) originate through a number of different mechanisms and that the latter are intimately related to the **DNA** organization of the **genes**, are now well-documented. Further, spontaneous mutations include those that cause diseases through loss of function as well as gain of function of **genes**. In contrast, most radiation-induced mutations studied in experimental systems (although identified through the phenotypes of the marker **genes**) are predominantly multigene deletions which cause loss of function; the recoverability of an induced deletion in a livebirth seems dependent on whether the **gene** and the genomic region in which it is located can tolerate heterozygosity for the deletion and yet be compatible with viability. In retrospect, the successful mutation test systems (such as the mouse specific locus test) used in radiation studies have involved **genes** which are non-essential for survival and are also located in genomic regions, likewise non-essential for survival. In contrast, most of the human **genes** at which induced mutations have been looked for, do not seem to have these attributes. The inference therefore is that the failure to find induced germline mutations in humans is not due to the resistance of human **genes** to induced mutations but due to the structural and functional constraints associated with their recoverability in livebirths. Since the risk of inducible genetic diseases in humans is estimated using rates of "recovered" mutations in mice, there is a need to introduce appropriate **correction factors** to bridge the gap between these rates and the rates at which mutations causing diseases are potentially recoverable in humans. Since the whole genome is the "target" for radiation-induced genetic damage, the failure to find increases in the frequencies of specific single-**gene** diseases of societal concern does not imply that there are no genetic risks of radiation exposures: the problem lies in delineating the phenotypes of recoverable genetic damage that are recognizable in livebirths. Data from studies of naturally-occurring microdeletion syndromes in humans and those from mouse radiation studies are instructive in this regard. They (i) support the view that growth retardation, mental retardation and multisystem developmental abnormalities are likely to be among the quantitatively more important adverse effects of

radiation-induced genet[redacted] damage than mutations in a fe[redacted] elected **genes** and (ii) underscor[redacted] the need to expand the focus [redacted] risk estimation from known genetic diseases (as has been the case thus far) to include these induced adverse developmental effects although most of these are not formally classified as "genetic diseases". In absolute terms, however, the risk of adverse developmental effects (as extrapolated from mouse data) is still small and can be reconciled with the lack of demonstrable increases in untoward pregnancy outcomes in human studies (given the combination of radiation doses and sample sizes). Note that most of these adverse developmental effects are here assumed to be related to recoverable deletions or other gross changes induced in the genome and are predicted to show, by and large, autosomal dominant patterns of inheritance; their genetic basis, therefore, is not the same as that of many naturally-occurring congenital abnormalities which are interpreted as being multifactorial in origin.

L6 ANSWER 3 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:510 BIOSIS
DN PREV199800000510
TI Preservation of blood and tissue samples for stable-carbon and stable-nitrogen isotope analysis.
AU Hobson, Keith A. (1) ; Gibbs, H. Lisle; Gloutney, Mark L.
CS (1) Canadian Wildlife Serv., 115 Perimeter Road, Saskatoon, SK S7N 0X4 Canada
SO Canadian Journal of Zoology, (Oct., 1997) Vol. 75, No. 10, pp. 1720-1723. ISSN: 0008-4301.
DT Article
LA English
SL English; French
AB Researchers engaged in collecting animal material for stable-carbon and stable-nitrogen isotope analysis are frequently faced with the need to preserve tissues prior to transportation to the laboratory. In many cases, freezing is not possible in the field, so we investigated the potential of several techniques for preserving tissues for this purpose. We also included preservation techniques used for **DNA** analyses in order to evaluate how they might alter deltal3C and deltal5N values in tissues and, ultimately, whether archived **DNA** samples could be used for stable-isotope **assay**. Tissues included blood and pectoral muscle from quail (Coturnix coturnix japonica) and blood from sheep (Ovis aries). Preservation techniques for blood included freeze-drying (control), drying on precombusted glass-fibre filter paper, and storing in 70% ethanol, 10% buffered formalin, ABI lysis buffer, and Queen's lysis buffer. After 6 weeks, the use of both lysis buffers and formalin resulted in significant depletion of 13C and 15N in blood. Values for samples dried on glass-fibre filter paper or stored in 70% ethanol did not differ significantly from those for the control. Muscle tissue was freeze-dried (control) or stored in 70% ethanol, 10% buffered formalin, or DMSO solution. Both the DMSO and formalin treatments resulted in significant depletion of 13C and 15N compared with the control. Only the 70% ethanol treatment did not result in changes to either isotope ratio in muscle. Where freezing is not possible, we recommend that blood samples be dried or stored in 70% ethanol. Our study provides an estimate of isotopic **correction factors** that may be applied to tissues archived for **DNA** analysis or stored in formalin.

L6 ANSWER 4 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1997:67518 BIOSIS
DN PREV199799906721
TI Comparison of plasma virus loads among individuals infected with hepatitis C virus (HCV) genotypes 1, 2, and 3 by Quantiplex HCV RNA **assay** versions 1 and 2, Roche Monitor **assay**, and an in-house limiting dilution method.
AU Hawkins, A.; Davidson, F.; Simmonds, P. (1)
CS (1) Dep. Medical Microbiol., Univ. Edinburgh, Teviot Place, Edinburgh EH8 9AG UK
SO Journal of Clinical Microbiology, (1997) Vol. 35, No. 1, pp. 187-192. ISSN: 0095-1137.
DT Article
LA English

AB The accuracy of different methods for the quantitation of hepatitis C virus in plasma was measured with samples from individuals infected with different genotypes and by using RNA transcripts of predetermined concentrations. Highly reproducible results were observed upon repeat testing of samples by both the original version of the Chiron branched-**DNA** (bDNA) **assay** (Quantiplex RNA **assay**; bDNA-1) and the currently available version (Quantiplex HCV RNA 2.0 **assay**; bDNA-2). A greater variability was observed in the Roche Monitor **assay** (correlation coefficient of 0.887, compared with 0.942 and 0.964 for the bDNA-1 and bDNA-2 **assays**, respectively). Significant differences in the efficiency of detection of genotypes 1, 2, and 3 were observed for the bDNA-1 and Roche Monitor **assays**, whereas the bDNA-2 **assay** and nested PCR at limiting dilution were able to quantify genotypes with equal sensitivity. By quantifying RNA transcripts of different genotypes, the sensitivities of the Roche Monitor **assay** for sequences of the type 1 and type 3 transcripts were estimated to be 21 and 8% of those achieved for genotype 2. When **correction factors** based upon these results and those from quantitation of circulating viral RNA sequences in samples from blood donors were used, the genotype-specific differences in virus load in samples from blood donors were no longer observed, consistent with previous studies with corrected values from the bDNA-1 **assay**. These results suggest that many of the previous studies evaluating the effect of genotype and virus load on the response to interferon using methods such as the Roche Monitor **assay** and other competitive PCR methods require reinterpretation. Differences in efficiency of quantitation should be taken into account in future investigations of the relationship between genotype and virus load.

L6 ANSWER 5 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:523521 BIOSIS
DN PREV199698245877
TI In line monitoring of intracellular ATP concentration in Escherichia coli fermentations.
AU Lasko, Daniel R.; Wang, Daniel I. C. (1)
CS (1) Dep. Chemical Eng., Massachusetts Inst. Technol., Cambridge, MA 02139 USA
SO Biotechnology and Bioengineering, (1996) Vol. 52, No. 3, pp. 364-372. ISSN: 0006-3592.
DT Article
LA English
AB A method was developed to provide a real-time measurement of intracellular adenosine 5'-triphosphate (ATP) concentrations in growing Escherichia coli. The bacteria to be monitored must first be modified by inserting the cDNA for firefly luciferase expressed from a constitutive promoter. Such a construct leads to constant specific activity of firefly luciferase during both the lag phase and exponential growth. When the luciferase substrate, D-luciferin, is added to the medium, ATP within the cells is utilized in the luciferase-catalyzed reaction that produces light. The light is carried from the bioreactor to a computer-based detector by an optical fiber. The detected per cell light emission varies during exponential growth. Analysis of cytoplasm extracts shows that this variance is related to changes in the ATP concentration, which ranges from 1 to 6 times the literature value for E-M. Experimental analyses demonstrated that inner filter effects are not a significant factor affecting the use of this system. The method was tested in a benchtop fermentor at cell densities above 13 g/L dry cell weight. A **correction factor** based on the accumulated light data is calculated and used in real time to account for consumption of luciferin from the culture broth by the light producing reaction. Dissolved oxygen concentrations must be kept above 15% of air saturation to ensure constant light output, but no detectable increase in oxygen demand is seen. The method does not significantly affect growth or production rates.

L6 ANSWER 6 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1994:497820 BIOSIS
DN PREV199497519820
TI Variance to mean ratio, R(t), for poisson processes on phylogenetic trees.
AU Goldman, Nick

CS Lab. Mathematical Biol[redacted] National Inst. Med. Res., Ridgeway, Mill Hill London NW7 1AA UK
SO Molecular Phylogenetics and Evolution, (1994) Vol. 3, No. 3, pp. 230-239. ISSN: 1055-7903.
DT Article
LA English.
AB The ratio of expected variance to mean, R(t), of number of **DNA** base substitutions for contemporary sequences related by a "star" phylogeny is widely seen as a measure of the adherence of the sequences' evolution to a Poisson process with a molecular clock, as predicted by the "neutral theory" of molecular evolution under certain conditions. A number of estimators of R(t) have been proposed, all predicted to have mean 1 and distributions based on the chi-2. Various **genes** have previously been analyzed and found to have values of R(t) far in excess of 1, calling into question important aspects of the neutral theory. In this paper, I use Monte Carlo simulation to show that the previously suggested means and distributions of estimators of R(t) are highly inaccurate. The analysis is applied to star phylogenies and to general phylogenetic trees, and well-known **gene** sequences are reanalyzed. For star phylogenies the results show that Kimura's estimators ("The Neutral Theory of Molecular Evolution," Cambridge Univ. Press, Cambridge, 1983) are unsatisfactory for statistical testing of R(t), but confirm the accuracy of Bulmer's **correction factor** (Genetics 123: 615-619, 1989). For all three nonstar phylogenies studied, attained values of all three estimators of R(t), although larger than 1, are within their true confidence limits under simple Poisson process models. This shows that lineage effects can be responsible for high estimates of R(t), restoring some limited confidence in the molecular clock and showing that the distinction between lineage and molecular clock effects is vital. However, these results also indicate that R(t) may be a poor statistic for analyzing the accuracy of Poisson process models and the molecular clock and that tests based on the whole likelihood function are more suitable.

L6 ANSWER 7 OF 15 BIOSIS COPYRIGHT 2011 BIOSIS
AN 1994:435705 BIOSIS
DN PREV199497057[illegible]
TI Enzymatic **assay** for quantification of deoxynucleoside triphosphates in human cells exposed to antiretroviral 2',3'-dideoxynucleosides.
AU Gao, Wen-Yi [1]; Johns, David G.; Mitsuya, Hiroaki
CS [1] Exp. Retrovirol. Sect., Medicine Branch, Natl. Cancer Inst., Build. 10, Room 5A14, Bethesda, MD 20892 USA
SO Analytical Biochemistry, (1994) Vol. 222, No. 1, pp. 116-122. ISSN: 0003-2697.
DT Article
LA English
AB Quantification of intracellular 2'-deoxynucleoside-5'triphosphates (dNTPs) is of importance in studies of antiretroviral 2',3'-dideoxynucleoside analogs (ddNs) and a highly sensitive enzymatic **assay** for dNTPs has frequently been used for this purpose. However, the susceptibility of the **assay** to interference from the corresponding substrate analogs, ddNTPs, is still undefined. Ideally, **DNA** polymerases used in the **assay** should meet at least two criteria: (i) high fidelity to the template even in the presence of ddNTPs and (ii) low affinity for ddNTPs. None of the currently used exonuclease-free Klenow and Sequenase enzymes met both criteria. However, Sequenase had higher fidelity to the template than did the Klenow enzyme in the presence of pyrimidine-ddNTPs, and its reaction followed first order kinetics. We have, therefore relying primarily on Sequenase, designed a dNTP proportional reduction **assay** to correct the ddN-induced deviation in the enzymatic **assay**. With the use of high-fidelity exonucleasefree **DNA** polymerase and the application of **correction factors**, we now can accurately quantify dNTPs with a minimum detection limit as low as 0.1 pmol, using as few as 1 times 10-4 peripheral blood mononuclear cells. The method described should be useful in the study and development of antiretroviral ddNs.

L6 ANSWER 9 OF 15 BIOSIS COPYRIGHT 2011 BIOSIS
AN 1994:441451 BIOSIS

AN PREV199497154951
TI Fluorescence lifetime analysis of **DNA** intercalated ethidium bromide and quenching by free dye.
AU Heller, Dennis P.; Greenstock, Clive L. (1)
CS (1) Radiation Biol. Branch, AECL Res., Chalk River, ON K0J 1J0 Canada
SO Biophysical Chemistry, (1994) Vol. 50, No. 3, pp. 305-312.
DT Article
LA English
AB The fluorescence characteristics of ethidium bromide (Eb) complexed to calf thymus **DNA** have been examined using fluorescence lifetime analysis for a range of **DNA** (effective nucleotide concentration) to Eb molar ratios. Control of both temperature and ion concentration is necessary for reproducible analyses. Eb complexed to double stranded **DNA** has a maximum fluorescence lifetime of 1.8 ns and is easily distinguishable from a fluorescence lifetime value of 1.67 ns corresponding to unbound Eb. In a solution of calf thymus **DNA** containing excess Eb a binding equilibrium is reached, and this corresponds to one Eb molecule for every five nucleotides. With increasing amounts of unbound Eb, the fluorescence lifetime of the **DNA**-Eb complex decreases with a concomitant drop in the steady state fluorescence intensity, without a change in the amount of Eb bound to **DNA**. It is concluded that unbound Eb, acting via a quenching mechanism, shortens the fluorescence lifetime of bound Eb and consequently decreases the overall fluorescence intensity. This means that a different approach is necessary: time-resolved fluorescence spectroscopy directly distinguishes between a decrease in fluorescence intensity due to quenching by an excess of unbound Eb from that due to a decrease in Eb binding to double-stranded **DNA**. These studies suggest that techniques which measure total steady state fluorescence intensity of bound Eb in order to infer relative amounts of double-stranded **DNA** must be interpreted with caution. For such **assays** to be valid it is essential that no unbound Eb be present; otherwise a variable **correction factor** is required to account for unbound Eb.

L6 ANSWER 9 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1993:319688 BIOSIS
DN PREV199396035088
TI Optimum conditions for the **assay** of cardiac RNA: Comparative content and effect of hypertension.
AU Siddiq, Tahir (1); Richardson, Peter J. (1); Preedy, Victor R.
CS (1) Dep. Cardiol., King's Coll. Sch. Med., Dentistry, Bessemer Rd., London SE5 9PJ UK
SO Biochemical Medicine and Metabolic Biology, (1993) Vol. 49, No. 2, pp. 149-163.
ISSN: 0885-4505.
DT Article
LA English
AB An investigation was made into techniques for the routine measurement of cardiac ribonucleic acid (RNA). Conditions were defined for the determination of rat ventricular RNA, based on uv absorption spectrophotometry. Optimum RNA hydrolysis occurred at 0.3 mol/liter alkali at 37 degree C for 1 h. Suitable **correction factors** for non-RNA material were also described and these gave similar results to RNA assayed by colorimetric methods. It was concluded that many of the methods previously reported may cause artifactual observations (in some cases apparent negative amounts of RNA). The technique was applied to the **assay** of RNA in various regions of the heart (i.e., left and right atrial and the left and right ventricular regions) and compared with noncardiac tissues (i.e., skeletal muscle, liver, bone, intestine, and kidney). The left ventricular RNA concentrations were comparable to the right ventricle and the interventricular septum, but approximately half that of atria. There were very little differences between left and right atrial regions. Differences between atrial and ventricular regions were reduced when data were expressed relative to **DNA**. The cardiac RNA content was shown to be comparable to skeletal muscle and bone. However, cardiac RNA concentrations were lower than those of kidney, liver, lung, and small intestine. Data were also expressed relative to **DNA** and showed that cardiac RNA/**DNA** ratios were higher than those of skeletal muscle and lower than those of bone, kidney, liver,

lung, and small intest[redacted]. The **assay** procedure for cardi[redacted] RNA was applied to investig[redacted]ions in the hypertrophied left [redacted]ntricle induced by aortic constriction. After 10 days the RNA concentration (mg/g wet wt) and RNA content (mg/region) increased by 7 and 43 %, respectively.

L6 ANSWER 10 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1987:210384 BIOSIS
DN BA83:1:8014
TI INTERPRETATION OF THE LYMPHOID MODULATION IN THE FOLLICULAR CENTER A MORPHO-PHOTOMETRIC **ASSAY** OF STORED SLIDES STAINED WITH HEMATOXYLIN-EOSIN.
AU ESQUIVAS C J; DEL MORAL R G
CS LOPEZ-QUEVEDO, SERV. ANATOMIA PATOLOGICA. HOSP. "VIRGEN DE LAS NIEVES", GRANADA.
SO SANGRE (BARC), 1986 (REC'D 1987)) 31 (5), 521-533.
CODEN: SNGRAX. ISSN: 0036-4355.
FS BA; OLD
LA Spanish
AB A photometric study of the different lymphoid cells comprised in the germinal centre was performed with a MPV2 Letiz photometer on stored slices from reactive lymph nodes, the nuclear size being also measured with a micrometric eyepiece. Original **correction factors** were introduced in order to homologate the measurements achieved. Different mean values were obtained ($p < 0.05$) when comparing the morphometric and photometric values of each cell type with the remaining ones. The smallest nuclear size corresponded to lymphocytes (4.67 microns) and the largest one was that of immunoblasts (8.93 microns). After arranging cell nuclei in accordance with their absorption, they were found to keep a sequence similar to that of the cell maturation pattern described by Lukes-Collins and Taylor. The values of nuclear extinction of small and large centrocytes (1.0 and 0.93) are one half that of the lymphocytes and immunoblasts (1.82 and 0.68, respectively). These findings that led us, in H-E stained slides, to identical interpretation of the morpho-functional lymphoid modulation than that attained through tritiated thymidine studies. Thus, data achieved by both methods allow us to assume that observed cells are in the S phase and contain amounts of **DNA** intermediate between that of the G1 cells (lymphocytes) and M phase cells (large centroblasts, immunoblasts).

L6 ANSWER 11 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1986:224149 BIOSIS
DN BA81:115449
TI **CORRECTION FACTORS** FOR THE DIPHENYLAMINE TEST FOR **DNA** IN YEASTS.
AU SUBDEN R E; KRICUS A
CS DEP. BOTANY GENETICS, UNIV. GUELPH, GUELPH, ONT. N1G 2W1, CAN.
SO MICROBIOS, 1985 (REC'D 1986)) 43 (176S), 233-244.
CODEN: MCBIAT. ISSN: 0026-1643.
FS BA; OLD
LA English
AB The diphenylamine **assay** for **DNA** content of yeast in unsatisfactory due to the presence of a yeast component which inhibits the colour reaction. The inhibitor is found in a wide range of yeast species and has not been identified. The relationships between the degree of inhibition and cell concentration, temperature an time of hydrolysis and extraction have been described. A formula for correction of the inhibition has been derived.

L6 ANSWER 12 OF 15 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1985:397621 BIOSIS
DN BA80:67613
TI SIGNIFICANCE OF SIMILARITIES IN PATTERNS AN APPLICATION TO BETA INTERFERON-RELATED **DNA** ON HUMAN CHROMOSOME 2.
AU MAY L T; LANDSBERGER F R; INOUYE M; SEHGAL P B
CS ROCKEFELLER UNIVERSITY, NEW YORK, N.Y. 10021.
SO PROC NATL ACAD SCI U S A, 1985 82 (12), 4091-4194.
CODEN: PNASA6. ISSN: 0027-8424.
FS BA; OLD
LA English

AB The nucleotide sequence of a 14-kilobase (kb) region of the human .beta. interferon (IFN-.beta.)-related **DNA** locus on chromosome [redacted] (genomic **DNA** clone .lambda.B3) was determined and compared to that of the IFN-.beta.1 **gene** by using the Sellers TT algorithm. This algorithm aligns segments of 1 sequence with similar segments in a 2nd sequence. A strategy was developed for assessing the significance of similarities between **DNA** sequences based on a scheme that recognizes patterns or runs of identities within an alignment. The pattern score (.PI.) thus obtained is an entropy-like measure. Numerically it is a reflection of the length of the 2nd longest run of identity in an alignment plus a **correction factor** due to the other shorter identity runs in the alignment. When the IFN-.beta.1 **gene** is compared to a random nucleotide sequence, the distribution of .PI. scores in such comparisons fits a Gaussian function. This strategy was used to identify 7 segments along one strand of .lambda.B3 **DNA** that are related to segments in IFN-.beta.1; these 7 alignments have .PI. scores .gtoreq. 3 standard deviations above the mean score obtained in comparisons between IFN-.beta.1 and random nucleotide sequences. One of those alignments (section 7) has a .PI. score 8.1 standard deviations above this mean score. The likelihood of finding an alignment statement as good as that in section 7 in a random sequence the length of the human genome is .apprx. 10-7. The .lambda.B3 **DNA** sequence in section 7 selects the human IFN-.beta.1 **gene** as the most significant alignment in computer searches of mammalian nucleotide sequence data banks.

L6 ANSWER 13 OF 15 MEDLINE
AN 96404193 MEDLINE
DN 96404193
TI Accurate and absolute quantitative measurement of **gene** expression by single-tube RT-PCR and HPLC.
AU Hayward-Lester A; Oefner P J; Sabatini S; Doris P A
CS Department of Cell Biology and Biochemistry, Texas Tech University Health Sciences Center, Lubbock 79430, USA.
NC DDK35385 (NHGRI)
IP01-HG00005
DDK36118
SO GENOME RESEARCH, (1995 Dec) 5 (6) 494-99.
Journal code: CES.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199701
AB We report a method that allows accurate, absolute quantification of **gene** expression in a single reverse transcriptase (RT)-PCR reaction. This method makes use of novel high-performance liquid chromatography (HPLC) technology to resolve and quantify the products of competitive, mutant RNA PCRs. The HPLC technique allows rapid, high resolution of reaction products. On-line UV detection eliminates the need for radiolabel or other tracers. The HPLC technique also demonstrates that those competition reactions readily generate heteroduplex products. The ability of HPLC to resolve and quantify heteroduplex products is fundamental to the accuracy of the technique. Accurate measurements of **gene** expression have been obtained over four orders of magnitude and experiments employing predetermined quantities of specific native RNA input have demonstrated the ability of the system to provide absolute estimates of **gene** expression. Large size differences between native and mutant RNA inputs affected reverse transcriptase (RT) efficiency, but not PCR amplification efficiency. However, the magnitude of the RT efficiency effect can be estimated, is reproducible, and can therefore be adjusted by a calculated **correction factor**. The RT efficiency difference can been eliminated by reduction in the magnitude of the sequence difference between native and mutant RNA so that no **correction factor** is required. The application of the technique to quantification of expression of the alpha 1 subunit of sodium, potassium-ATPase in microdissected nephron segments is demonstrated.

L6 ANSWER 14 OF 15 MEDLINE
AN 85056916 MEDLINE
DN 85056916
TI Cell division does not affect Sendai virus genome replication in persistently infected BHK cells.
AU Portner A; Beffy P
SO JOURNAL OF GENERAL VIROLOGY, (1984 Nov) 65 (Pt 11) 2055-60.
Journal code: I9B. ISSN: 0022-1317.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 198503
AB The extent of Sendai virus genome replication in persistently infected BHK cells actively growing or at confluence was followed by estimation of the [3H]uridine incorporated into intracellular nucleocapsid RNA. First, we showed that, in the presence of actinomycin D, actively growing persistently infected cells were taking up threefold more [3H]uridine than resting cells. This higher uptake exhibited by growing cells was observed neither in persistently infected cells in the absence of actinomycin D, nor in acutely infected cells in the presence of actinomycin D. Assuming that the cellular pool of unlabelled uridine stays constant, we used a **correction factor** for this difference in [3H]uridine uptake and estimated [3H]uridine incorporation in nucleocapsid RNA, normalizing the data either to the amount of cell or of viral template. Results showed that the viral genome replication, expressed either way, was not significantly influenced by cell growth conditions.

L6 ANSWER 15 OF 15 SCISEARCH COPYRIGHT 2001 ISI (R)
AN 96:371329 SCISEARCH
GA The Genuine Article (R) Number: UK963
TI DOSE-RESPONSE CURVES FOR SIMPLE AND COMPLEX CHROMOSOME-ABERRATIONS INDUCED BY X-RAYS AND DETECTED USING FLUORESCENCE IN-SITU HYBRIDIZATION
AU SIMPSON P J (Reprint); SAVAGE J R K
CS MRC, RADIAT & GENOME STABIL UNIT, CHROMOSOME DAMAGE GRP, HARWELL DX11 0RD, BERKS, ENGLAND (Reprint)
CYA ENGLAND
SO INTERNATIONAL JOURNAL OF RADIATION BIOLOGY, (APR 1996) Vol. 69, No. 4, pp. 429-436.
ISSN: 0955-3002.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 35
ABSTRACT IS AVAILABLE IN THE ALL AND TALL FORMATS
AB A primary human fibroblast cell-line was grown to confluence and X-irradiated at 2, 4 and 6 Gy. The resulting chromosome aberrations were detected in first-division cells using a series of FISH **assays** in which either one or two chromosomes (nos. 1, 2, 4, 5, 7 and 13) and all centromeres were painted with distinct colours. Interchange aberrations were classed as simples if they appeared to originate from a break in each of two chromosomes (dicentric with fragment or reciprocal translocation), or complexes if their origins required three or more breaks in two or more chromosomes. Breaks not obviously connected with exchanges were also scored. The data were corrected to include paint patterns resulting from either incomplete or terminal exchanges. In addition we attempted to correct for the apparently simple exchanges which are actually derived from complex interactions (pseudosimples) using **correction factors** calculated by establishing the predominant complex families present at each dose. Power Law analysis of the corrected data showed a linear dose-response for simple exchanges and a dose-squared response for complex exchanges. Based this observation we suggest that simples result lesions induced by the same radiation track and complexes arise from the interaction of lesions induced by separate tracks.

=> d his

FILE 'HOME' ENTERED AT 16:19:54 ON 01 FEB 2001

FILE 'BIOSIS, CAPLUS, MEDLINE, SCISEARCH' ENTERED AT 16:19:14 ON 01 FEB 2001

L1 39 S (FILTER OR ARTIFACT OR ANOMAL?) AND ((GENE ARRAY) OR (GENE CH
L2 17 DUP REM L1 (21 DUPLICATES REMOVED)
L3 12926 S (CORRECTION FACTOR)
L4 39 S L3 AND (DNA) AND (GENE OR ARRAY OR CHIP OR ASSAY)
L5 19 DUP REM L4 (24 DUPLICATES REMOVED)
L6 15 S L5 NOT L2